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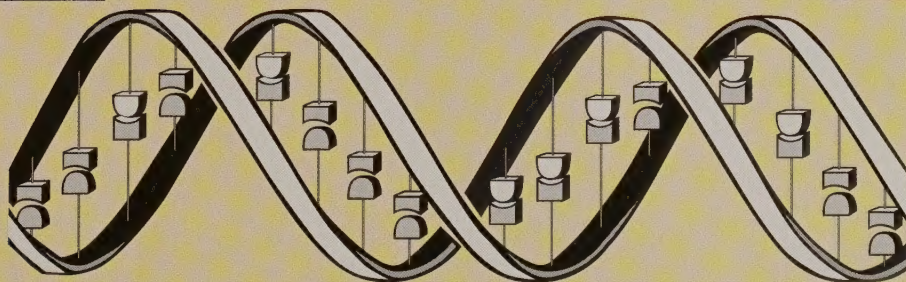
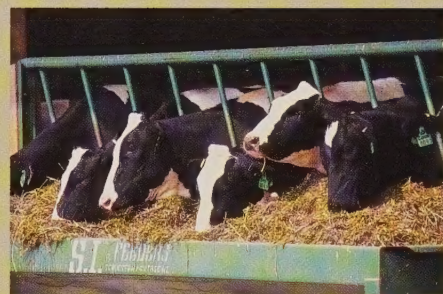
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United States Department of Agriculture
Agricultural Research Service

Food Animal Production Program

Research
Highlights
2000-2005



Foreword

This *Agricultural Research* magazine reprint contains articles published from January 2000 to February 2005 addressing research conducted at various area research units and experimental stations as part of the U.S. Department of Agriculture, Agricultural Research Service's Food Animal Production Program.

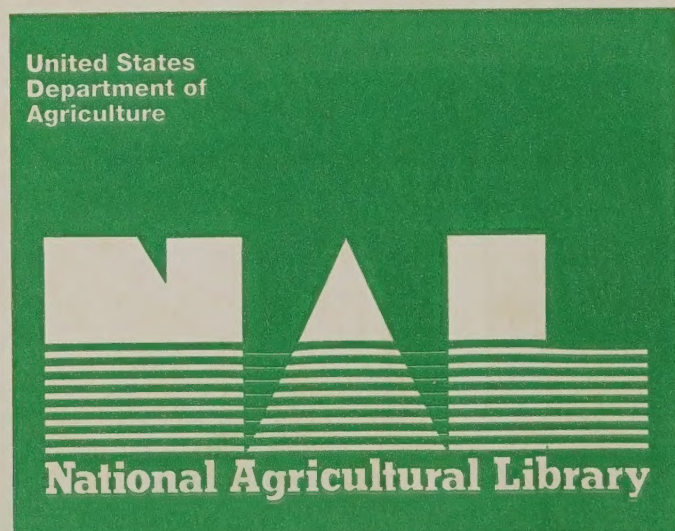
The mission of the Food Animal Production Program is to protect, evaluate, identify, and develop biotechnological methods to use animal germplasm and associated genetic and genomic repositories and databases to ensure an abundant and safe supply of animal products at a price that is competitive in the United States and foreign markets.

The current research components of this program include the following:

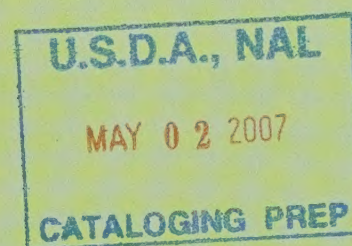
- Reproductive efficiency
- Conservation, characterization, and use of genetic resources
- Genetic improvement
- Genomics tools
- Nutrient intake and use
- Growth and development
- Product quality
- Integrated systems

The program currently includes 45 research projects supported by 91 scientists located at 17 research sites throughout the United States. The program is led by Ronnie D. Green, National Program Leader, Animal Production, and Lewis Smith, National Program Leader, Aquaculture and Animal Well-Being. For additional information about the national programs and the more than 1,200 research projects carried out by USDA's Agricultural Research Service (ARS), visit www.ars.usda.gov/research/programs.htm.

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Cover: A montage of different species represented in the Food Animal Production National Program: beef cattle, dairy cattle, sheep, swine, and poultry.

Finding Out What Makes Animals Tick—Genetically

Since Watson and Crick first discerned the structure of DNA 50 years ago, scientists have been studying it, hoping to unravel the mysteries of animal and plant growth and reproduction. Agricultural scientists have constantly sought to put the burgeoning knowledge to practical purposes, breeding animals with natural resistance to disease or ones that produce more efficiently.

In the beginning, decoding the series of genes that make up DNA strands, unique to each living organism, was very slow and tedious. In the early 1980s, tools such as polymerase chain reaction and short tandem repeat DNA markers started us in the right direction.

The late 1980s and early 1990s saw DNA technology evolve rapidly, thanks to large amounts of money being dedicated to human genome study. A genome is all the genetic information or hereditary material possessed by an organism. Scientists hope that by learning about the genes that make a human being—and the roles they play in health and growth—it may be possible one day to cure hereditary problems, such as Tay-Sachs disease, various forms of cancer, and Parkinson's.

Concurrently, scientists in the animal-research community began working with counterparts involved in human genomic studies. The quality and speed of DNA analyses were aided by development of improved, automated sequencing technology. Greater computer capabilities and specialized software made it feasible for researchers to manage the huge amount of data generated by DNA analyzers, doing in days or weeks what previously took months in a laboratory.

Today, with agencies and universities from several countries helping to conduct it, animal genomic research has become a worldwide effort. One of my responsibilities is to represent ARS and USDA as a member and executive secretary of the Interagency Working Group on Domestic Animal Genomics. The group, formed in 2002, coordinates the genomic research of eight U.S. federal agencies through the National Science and Technology Council, a cabinet-level council that creates science and technology policy for the U.S. government.

For fiscal year 2004, Congress appropriated more than \$33 million for ARS's animal genomics research. It represents a great investment in the agency that has already quickened the pace of genomics research. Soon, research that took 10 years to complete in the 1980s may be completed in just a few years. And application of this new knowledge may range from producing consistently tender steaks to preventing human diseases.

Scientists are now—or shortly will be—sequencing the genomes of the cow, pig, honey bee, and chicken. This work

will help to pinpoint all the genes and, eventually, the various functions they govern. Sequence maps will make it possible to more easily unravel interactions between genes. Quantitative geneticists have theorized for decades that it's these interactions that create the phenotypic effects that are economically important.

Many animals are genetically similar to each other. Sheep and goats are ruminants and are genomically similar to cows. Likewise, turkeys are similar to chickens. So researchers already have the advantage of knowing a lot about these animals without having to spend time and money physically mapping the location of each and every gene.

The Interagency Working Group is beginning to explore the possibility of sequencing the catfish, rainbow trout, and Pacific oyster. Nonagricultural animals, such as the mouse and dog, have already been mapped by other groups. Agency researchers are able to access and use this information as well.

The article beginning on page 4 illustrates the genomic work that ARS—with collaborators from around the world—has already accomplished with these animal species. The objectives of genetics and genomics research extend far beyond the traditional goal of producing adequate quantities of safer, better, and cheaper food. Completed maps will allow scientists to compare the genetic makeup of these agriculturally important animals to learn more about each of them—and to learn more about humans.

They will also learn ways to improve the health and well-being of farm animals. In an age of bioterrorism threats, it is also necessary to understand the genes that will react if livestock are ever endangered by biological agents.

The National Institutes of Health is a major collaborator with ARS, particularly because of the potential human health benefits that may arise from animal genomic research. For example, completion of the chicken genome will provide a valuable model for human embryology and development as well as for study of reproductive diseases. It should also help to expand knowledge of cancer and other diseases. Researchers study the honey bee because it's a good model for aging. Scientists want to study the honey bee's nervous system as well.

ARS continues to be highly interested in research to produce more efficient animals. Tools developed from genomics research will allow better identification of the proper animal for any particular production system and environment. That will lead to more efficient raising of higher quality meat animals at lower prices to the American and worldwide consumer.

Ronnie D. Green

ARS National Program Leader
Food Animal Production
Beltsville, Maryland

Chinese Pigs Provide Insight to U.S. Swine Reproduction

Some say the animal is so cute. Others say it is the funniest-looking thing they've ever seen. Either way, scientists in the United States were delighted to obtain some for research in the late 1980s.

They are the Meishan (pronounced MAY-shawn) pigs of southern China. They were always known for their large litters (15-16 piglets compared to 10-12 for U.S. sows). Researchers from various countries wanted to find out why this occurred.

The first Meishan pigs (and a few other Chinese-bred pigs) were brought to the United States in 1989. After being quarantined in Florida, they were delivered to ARS' Roman L. Hruska U.S. Meat Animal Research Center (MARC) in Clay Center, Nebraska; the University of Illinois; and Iowa State University.

Initially, researchers were interested only in the females; male Meishans were brought along simply to help produce more females, says MARC animal physiologist Joe Ford. Scientists hypothesized that elevated levels of follicle-stimulating hormone (FSH) in Meishan females were the cause of their large litters. But the researchers found that FSH levels in Meishan females were similar to those in U.S. females, says Gary Rohrer, a geneticist at MARC.

After further study, they found that Meishan females begin puberty in only 60 days, much earlier than other pigs. They also ovulate more eggs per cycle and have a greater uterine capacity to deliver more live piglets.

Eventually the researchers started studying the males and learned some interesting facts about their reproductive organs, too. The first important finding was that Meishan boars have five to seven times more FSH in their blood than U.S. boars have, but their testes were 40 percent smaller than those of U.S. boars.

The small size reflects the finding that Meishan boars have fewer Sertoli cells—the cells that develop sperm—in their testes. So, fewer Sertoli cells means less sperm and, curiously, more FSH. But how this mechanism relates to litter size or to other reproductive traits is still under study.

ARS researchers also found that a gene (or genes) on the X-chromosome affects the size of Meishans' testes, whereas in rodents, testis size is more affected by the genes on the Y-chromosome.

Scientists like the fact that Meishans provide a new and different model to investigate swine sperm production. Ford says that since 75 percent of newborn pigs in the United States are produced through artificial insemination, finding ways to improve sperm production is important to improving the efficiency of U.S. pork production.

KEITH WELLER (K10089-2)



Geneticist Gary Rohrer examines Meishan pigs at the ARS Roman L. Hruska U.S. Meat Animal Research Center in Clay Center Nebraska.

Pork products from Meishans taste as good as those from conventional breeds, but Meishan meat has more fat. Ford says his laboratory is using the Meishans only as an experimental model to compare to other breeds of pigs. They are not very useful for crossbreeding, but their unusual characteristics help scientists study biological processes in traditional pigs.—By **David Elstein**, ARS.

This research is part of Food Animal Production, an ARS National Program (#101) described on the World Wide Web at <http://www.nps.ars.usda.gov>.

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KEITH WELLER (K10089-4)



Mapping the Way to Disease-Free Chickens

“The poultry industry is afraid it may start losing the vaccine race against Marek’s disease, as ever more virulent strains appear and cause unbearable losses.”

—Hans Cheng

The newest version of a chicken genome map gives Hans H. Cheng hope for developing a chicken resistant to Marek’s disease, a viral disease that causes tumors in the birds.

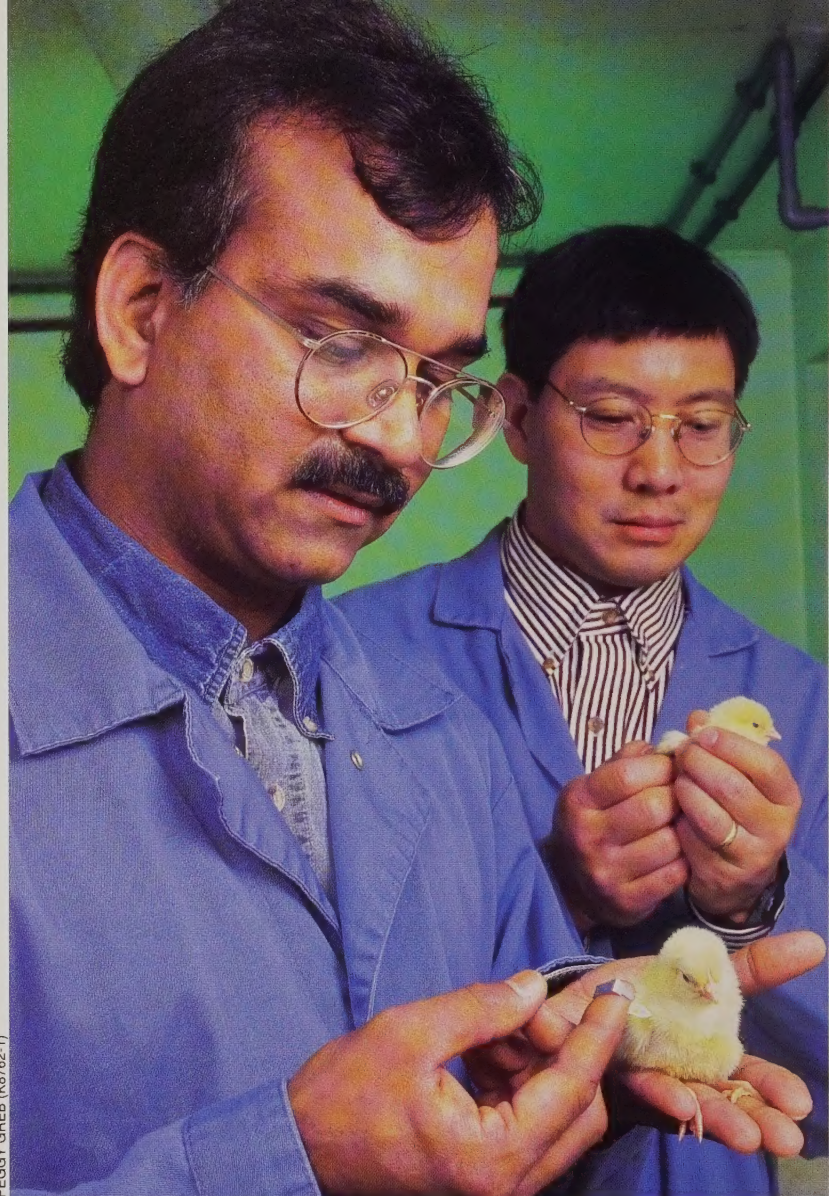
“The poultry industry is afraid it may start losing the vaccine race against Marek’s disease, as ever more virulent strains appear and cause unbearable losses,” says Cheng, a geneticist with USDA’s Agricultural Research Service. “That’s why using a genome map as a guide or road map to breeding chickens resistant to Marek’s disease is a priority.”

Before the first vaccine was developed in the late 1960s by scientists at the ARS Avian Disease and Oncology Laboratory in East Lansing, Michigan, the disease caused losses of \$300 million a year. Those losses came from a combination of deaths, fewer eggs, and condemnation of carcasses at poultry slaughter plants. Even with the vaccine, losses can still run as high as \$100 million a year.

The vaccine has to be updated periodically, in a race to keep ahead of ever more virulent strains. Cheng is counting on the genome map to help win the race.

“Chickens bred to resist Marek’s would be the first generation bred with modern molecular techniques,” Cheng says.

“The genome map will also help us build a superchicken, by helping us find the best combination of genes and proteins for resistance to many diseases as well as for productivity,” Cheng



PEGGY GREB (K8762-1)

▲ Farm manager Raj Kulkarni (left) and geneticist Hans Cheng examine a day-old chick for disease resistance and susceptibility. Each chick is tagged with a wing band for identification.

▼ Research associate Hsiao-Ching Liu prepares a sample of chicken RNA. The samples are then run on DNA microarrays to screen thousands of genes simultaneously. This new technology is especially promising and should lead to the rapid identification of agriculturally important genes.

PEGGY GREB (K8768-1)



says. Although their focus is on Marek's first and then other diseases, Cheng and his colleagues are also searching for genes that will promote better and more efficient growth.

The latest map can be viewed on the WWW at <http://poultry.mph.msu.edu/resources/conmap/conmap.htm>. It is actually a composite of three maps, including one jointly constructed by the Avian Disease and Oncology Laboratory and its neighbor, Michigan State University in East Lansing. The other two maps come from the Compton Institute for Animal Health in England and the Wageningen Agricultural University in the Netherlands. The new map is the product of the International Chicken Genome Mapping Project begun in 1994.

Overlapping Maps

"This is the first such international effort," Cheng says, although individual countries such as the United States have worked on mapping chicken genes since 1936. "Chickens were the first farm animal to have their genes mapped. But, in the beginning, mapping was based on visible physical characteristics such as feather color, rather than today's biotechnology that allows DNA and RNA analysis."

PEGGY GREB (K8763-1)



Cheng, one of the co-coordinators of the East Lansing map project, along with Jerry B. Dodgson, a microbiologist at Michigan State, says the DNA samples used in making these maps come from the East Lansing lab and the Compton Institute.

The East Lansing lab sends these DNA samples around the world; they were taken from the blood of 52 chicks that were specially bred in 1990. The Compton Institute likewise sends vials of DNA samples around the world that are taken from a similar "reference family" of chicks. The samples were collected years ago and only from those individual chicks.

"So," Cheng says, "the DNA samples are in limited supply. But modern molecular techniques have greatly reduced the amount of DNA needed for mapping, so there no longer seems to be a danger of running out of samples."

All three maps used for the latest composite are genetic maps. The Compton Institute published the first such map. Dodgson is a few years away from a more detailed genome map. It is

called a physical map because the breakpoints used to map genes are produced by a physical cutting of DNA fragments from chromosomes. This contrasts with the genetic map in which the breakpoints occur naturally, as a result of sexual reproduction. A physical map fine-tunes a genetic map, giving a higher resolution—like a more detailed street map.

Cheng says that mapping a genome is like mapping a city neighborhood. "First you need to use street signs as markers, then you go looking for individual houses or genes," he says.

"We have about 2,000 genetic markers to help us locate genes," says Cheng. "For chickens, somewhere between 2,000 and 4,000 genetic markers is a reasonable goal to begin to construct a genome map and locate genes. The problem is that about half of these markers have limited utility because they can only map an individual chicken's genome and that of its progeny. Unlike the rest of our markers, these markers don't always mark the same gene in the same spot for all other chickens," he says.

When Dodgson's physical map is ready, it or a composite version will be integrated with the composite genetic map. Overlapping the maps helps build a better genome map.

"Every time one researcher finds another marker, another street sign is found for the maps," Cheng says. Different maps are lined up to provide guides for where to go next to complete the map. A physical map may be deficient in markers so we can use a genetic map to find those markers and vice versa."

All Creatures, Great and Small, Share Some Identical Genes

The maps also benefit from being overlaid with those of the human genome and other animal species.

"It's surprising how well the human and avian genomes line up," Cheng says. The human genome and chicken genome projects complement each other. By lining up the two maps, human immunologists and avian health researchers can help locate genes for traits that improve disease resistance in both species.

"The amazing thing about evolution is that it leaves many species—from yeast to mammals—sharing some of the same large chunks of DNA," Cheng says. "The same mapping

Cheng says that mapping a genome is like mapping a city neighborhood. "First you need to use street signs as markers, then you go looking for individual houses or genes."

techniques work in all species—plants and animals—with nuances caused by differences in biology and reproduction, for example.”

Since tumors are so common in chickens, the first cancer-causing genes were isolated from chicken tumor tissue. A gene that causes cancer in chickens will have similarities to a gene that causes cancer in humans. The East Lansing avian lab contributed greatly to the work on human cancer in the 1970s.

The Ultimate Science

Collaboration among geneticists—sharing and comparing of genetic maps—is typical of how scientists often work together to discover something, Cheng says. And collaboration is particularly needed in genome mapping.

“In that sense, genome mapping is the ultimate science. We’re all forced to collaborate, and we benefit from others’ work,” he says.

“The final step, after the maps are made and all the genes are sequenced, is to identify genes that influence the trait you’re looking for—in this case resistance to Marek’s disease,” says Cheng.

As a practical matter, Cheng and his colleagues in effect work on all these steps somewhat simultaneously. They are drawing the map at the same time as they are driving city streets and looking for house addresses.

“We take the maps we have and use them to sequence and identify genes with resistance to Marek’s,” he says. He recently began a new DNA technique called microarray to find these genes. “It should pare years off the search,” he says.

The microarray technique allows a search for a great number of genes at one time, rather than for gene markers, Cheng says.

PEGGY GREB (K8766-1)



Technician Laurie Molitor (left) and research associate Christiane Hansen analyze chicken genetic markers using DNA sequencers. These semiautomatic machines increase the number of samples that can be processed per day and minimize human errors.

“RNA is put on two microscope slides. The genetic material on one slide might be from a disease-resistant chicken, with the other slide containing RNA from a susceptible one,” he explains.

“A quick check of such samples, en masse shows differing responses in RNA levels between the two. The differences show which genes may be responsible for the trait. We hope this new technology, combined with gene mapping, will enable the rapid identification of genes for disease resistance,” he says.

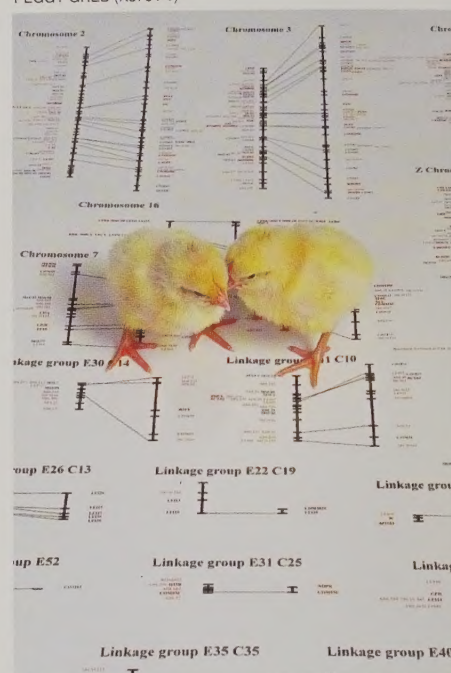
As another aid to gene identification, Cheng and his colleagues have also recently developed 19 inbred lines of chickens that have disease-resistance traits linked to one or a few genes, rather than to a complex of numerous genes. This makes identifying genes for disease resistance easier, and facilitates creating chickens that either are or are not disease resistant—nothing in between that would hamper the search, he says.

“This unique genetic resource will work for other traits as well, giving us the opportunity to quickly isolate the responsible genes,” Cheng adds.—By **Don Comis, ARS.**

This research is part of Animal Genomes, Germplasm, Reproduction, and Development, an ARS National Program (#101) described on the World Wide Web at <http://www.nps.ars.usda.gov/programs/appvs.htm>.

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PEGGY GREB (K8764-1)



Chicks atop a picture of a genetic map of a chicken. The chicken genome has 39 pairs of chromosomes, whereas the human genome contains 23 pairs.

Combining Traditional Practices and Modern Tools

Americans enjoy the safest, most abundant food supply on Earth. It's also the most affordable. The average American pays a little less than 11 percent of his or her disposable income on food—the lowest rate in the world. In 2002, it took only 39 days to earn enough to pay for food for an entire year. As recently as 1970, it took 51 days.

While housing and health care costs continue to rise, food has actually become more affordable. Why? Because of the efficiency and productivity of American farmers and ranchers. They're constantly fine-tuning their growing and breeding practices and using new technologies to boost their yields.

The Agricultural Research Service (ARS) plays a major role in developing the knowledge base and technologies that allow U.S. producers to meet consumer needs. For example, according to the Economic Research Service, the average American eats about 194 pounds of red meat, poultry, and fish in a year—16 pounds above the level eaten in 1970. Meeting such demands while keeping costs down and maintaining the quality consumers expect is no easy task.

In this regard, ARS has developed a Food Animal Production Action Plan. It supports improvements in reproductive and nutrient intake efficiency as well as product quality. The plan also supports conservation and use of genetic resources, development of genomic tools, and continued study of integrated systems and animal growth and development. With scientists stationed at labs across the United States, we look at questions related to these different areas and use the resulting data in ways that will serve producers and, ultimately, consumers.

Take the problem facing competing cattle producers in the Southeast. Thirty to 40 percent of the nation's beef cattle is produced there, and almost all these animals have some Brahman in their genetic makeup. Brahmans are more resistant to heat and pests than are breed types that evolved in more temperate climates. But they produce tougher steaks, and this can reduce consumers' satisfaction.

The ARS Subtropical Agricultural Research Station in Brooksville, Florida, is trying to overcome the Brahman toughness problem. Scientists are looking for genetic variation within the breed that would allow producers to choose sires based on the beef tenderness of their progeny and other characteristics. They have also started crossbreeding Angus, Brahman, and Romosinuano cattle to develop a line that imparts the benefits of a tropically adapted breed as well as improved carcass quality and reproductive efficiency.

Halfway across the continent, researchers at ARS' Roman L. Hruska U.S. Meat Animal Research Center in Clay Center, Nebraska, are using genetic diversity among sheep breeds to improve production efficiency. They are currently looking into streamlining sheep production systems by developing easy-care, meat-yielding breeds. One possibility they're exploring? Breeds of sheep that don't need to be sheared (see page 7).

The ARS National Animal Germplasm Program, based in Fort Collins, Colorado, is helping to preserve genetic diversity within food-animal populations. The program provides a safe repository for frozen semen or embryos from beef and dairy cattle, poultry, swine, sheep, goats, and aquatic animals. These genetic resources could help researchers solve future food-production problems.

ARS researchers are also using high-tech tools to improve food-animal production efficiency now. For instance, scientists at ARS' Biotechnology and Germplasm Laboratory in Beltsville, Maryland, are using techniques originally developed for human medicine to extend the viability of turkey sperm. The turkey industry relies on artificial insemination to produce nearly 300 million birds annually. Producers must inseminate breeder hens every week for 24 to 26 weeks, but they can store sperm for only 8 to 18 hours before it becomes infertile. Hens, however, can store viable sperm inside their bodies for more than 2 months. ARS researchers are hoping to identify the genes that allow hens to keep sperm alive by taking genetic "snapshots" of sperm-storage tissues from inseminated and noninseminated hens and comparing the two. Eventually, they may be able to use this information to create a method for storing viable sperm for days, weeks, or even months at a time.

Information systems help compile and quantify the massive amounts of production data collected on different animals. ARS researchers are harnessing the power of computer modeling to simulate production systems and uncover the economic value of different traits. As the article on page 12 indicates, modeling studies undertaken at Fort Keogh Livestock and Range Research Laboratory in Miles City, Montana, are helping producers find bulls that will produce the most profitable offspring.

Computers are also helping ARS researchers and others map the bovine, chicken, pig, sheep, and trout genomes, among others. When complete, these genetic road maps will provide additional information that researchers and producers can use to produce leaner, more tender, more fertile animals. Meantime, ARS will continue to combine traditional breeding programs with other tools at our disposal to sustain and increase food-animal productivity to benefit producers and consumers alike.

For more information about the ARS Food Animal Production Action Plan and the many research programs it comprises, visit the ARS National Program web site at www.nps.ars.usda.gov.

Joseph T. Spence

Acting Associate Administrator
Agricultural Research Service
Beltsville, Maryland

Mapping the Way to Bovine Bounty

Like road crews installing signposts on a long stretch of a highway, animal researchers are marking off regions of bovine DNA that will point the way to genes for a plethora of traits—from ideal body shape, ease of calving, and disease resistance, to protein-rich milk for dairy products.

And by inspecting the chromosomal housing for such DNA researchers aspire to use new means of predicting the inheritance of traits in offspring sired by prized bulls, or, by their semen samples, for that matter.

Yet, even with the artificial insemination of cows with such bull semen, dairy breeders must wait about 5 years before they can find out whether a bull calf will bear all the desired traits, says Melissa S. Ashwell. She's an animal geneticist at the ARS Gene Evaluation and Mapping Laboratory in Beltsville, Maryland. Her colleagues there are ARS geneticists Tad S. Sonstegard and Curtis P. Van Tassell.

With marker-assisted selection, a technique that would use the team's mapping information, timely genetic forecasts might be made from just a few embryo cells at a diagnostic lab, or using blood drawn from a newborn calf.

"If we had a particular marker, we should be able to predict from the embryo whether the desirable traits will be expressed. And even if you have to wait until that bull calf is born, you'd still save a lot of time and money versus waiting 5 years to see if the calf has the genetic potential to produce desirable dairy cows," says Ashwell.

Since the mid-1990s, her team has used mapping techniques to examine 150 to 200 different DNA markers from the semen of stud bulls—or sires—linked to 8 Holstein families. Each of these 8 patriarch bulls has sired at least 75 to 250 sons. The sons, in turn, fathered no less than 50 daughters.

Why the focus on Holsteins? "Their high milk production makes them the primary breed in the dairy industry," says Ashwell.

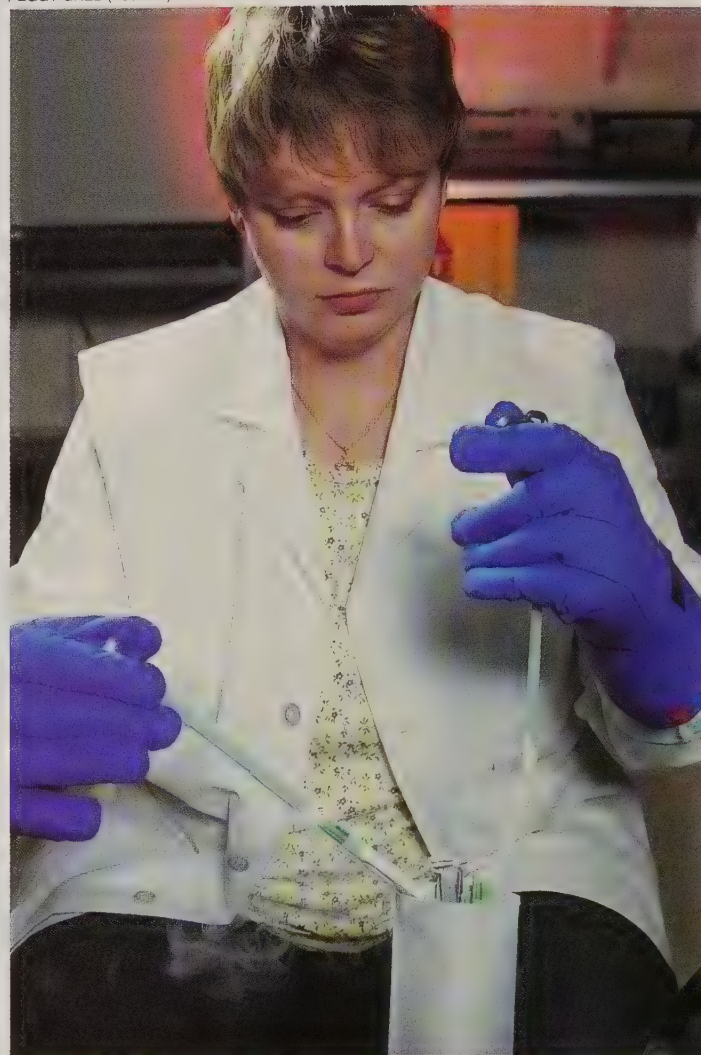
Marking a Territory—of DNA

For Ashwell and her co-workers, the search for important genes begins with an assortment of high-tech tools, including a high-throughput sequencer, and special probes called oligonucleotide primers. The latter finds and binds to genetic pieces of interest. Another tool is PCR. It's like a xerox machine that generates millions of copies of these DNA pieces—including marker regions—so they can be identified and sequenced.

"A marker is a very short stretch of DNA, probably 100 to 200 nucleotides long," Ashwell explains. It helps if you think of DNA as the alphabet that spells out an organism's traits and innermost workings. The nucleotides, then, are the chemical letters making up that alphabet. "The differences you see in markers are sequence differences in nucleotides," she says.

Using this technology, the Beltsville team in 1995 was first to stake a claim on a region of chromosome 23 where genes

PEGGY GREB (K8927-1)



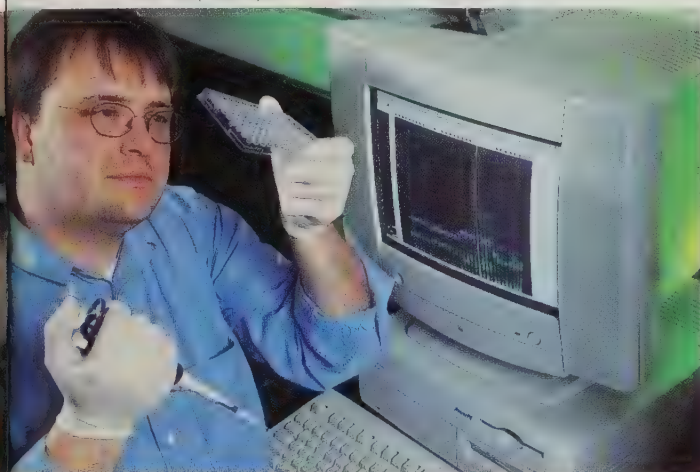
Animal geneticist Melissa Ashwell removes bull semen from a liquid nitrogen storage tank. DNA will be extracted from the semen and used for marker analysis.

may mediate a cow's response to mastitis. Susceptible animals can acquire this costly disease through *Staphylococcus* and other bacterial infections of their udder.

Dairy producers lose an estimated \$2 billion annually to the disease. Ideally, with marker-assisted selection techniques, commercial breeders could select for resistance traits based on such indicators as the animals' somatic (white blood) cell scores. This refers to the concentration of cells per milliliter of cow's milk. Ashwell cautions they're still uncertain how "statistically significant" the finding is and says it needs to be studied more in contemporary animals.

In the meantime, the team has taken their molecular prospecting to other chromosome regions. One of those, located on chromosome 27, is associated with "dairy form." This trait

PEGGY GREB (K8926-1)



Geneticist Tad Sonstegard prepares to load PCR samples onto an automated DNA sequencer.

SCOTT BAUER (K7963-1)



Information gained from mapping the genes of cows will one day be used to select dairy cows with greater milk production and improved disease resistance.

describes a cow's physical appearance, and may also be an indicator of ketosis, a metabolic disorder that typically affects cows with newborn calves. For ketosis, the scientists' goal is to come up with a fast, accurate method of identifying animals less likely to suffer the disorder.

Determining Traits Expressed by Genes

Whether dairy form or ketosis, the challenge for Ashwell and her colleagues is linking what's seen on chromosomes in the lab with physical evidence in the animals. In some cases, the team's findings run parallel to those of other researchers. At Pennsylvania State University, for example, geneticist Gary Rogers is investigating relationships among measures for body fat deposition and incidence of disease in dairy cows. Farther

west, at ARS' U.S. Meat Animal Research Center in Nebraska, geneticist Eduardo Casas is focusing attention on marbling traits in beef carcasses. Marbling affects the tenderness of meat cuts like steak and is associated with an animal's fat content. Based on this, Rogers' data, and marker work at Beltsville, "we think the same gene or gene cluster could be involved in marbling in beef cattle and fat content in dairy cows," reports Ashwell.

She is quick to credit the ongoing work of human genome mappers for helping them blaze the trail in bovine studies. Much of that's because animal researchers can extrapolate data from human genome mapping to zero-in on the equivalent on cow chromosomes.

For example, "using fluorescent tags, we use markers from bovine chromosome 27 (there are 29 total in cattle, plus the two sex chromosomes, X and Y) and see what region that corresponds to in human chromosomes," says Ashwell. "So much is known about human chromosomes—we try to feed off that knowledge and identify candidate genes that may explain the differences in dairy cattle."

But selecting these candidate genes isn't always easy. For example, the Beltsville team recently identified an association between DNA markers on chromosome 6 and the amount of protein in milk. Many of these milk proteins are called caseins.

"These genes would be obvious candidate genes that could have explained the differences we see in protein content," Ashwell says. "But the casein genes are located close to the chromosome's bottom, and we're seeing our effect at a different location on the chromosome much further up. This suggests that there are several different genes that affect important traits like protein content."

Eventually, information gleaned from this genetic riddle may offer a way for breeders to select animals whose milk contains even more protein. Casein proteins are especially important for cheesemaking. But some caseins are better suited than others to this. With the right genetic tools, Ashwell ventures, there may come a day when cows are bred for milk that contains specific proportions of these cheese-friendly proteins.

By marking off chromosome regions, scientists can begin creating a genetic roadmap that can be used to put desirable traits into cows. "If we can get this mapping technology perfected," says Ashwell, "we're going to breed better and better cows."—By **Jan Suszkiw**, ARS.

This research is part of Animal Genomes, Germplasm, Reproduction, and Development, an ARS National Program (#101) described on the World Wide Web at <http://www.nps.ars.usda.gov/programs/appvs.htm>.

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Minutes after giving birth, a 2-year-old cow attends to her newborn calf.

As far back as he can remember, Tom Mott has helped with calving. When he was young, he and his dad would place bets on which of the Herefords on their Utah ranch would calve first. “That’s how my dad taught me to watch heifers,” says Mott.

Heifers are females before they become mothers; after that, they’re called cows. A week or two before they’re ready to calve, Mott says, the heifers’ udders will tighten up with milk. Then, as they get ready to calve they will swish their tails and try to go off by themselves.

Mott’s family still runs a ranch, but he now works as a herdsman at ARS’ Fort Keogh Livestock and Range Research Laboratory (LARRL), in Miles City, Montana.

Once the pregnant heifer goes into labor and lies down, Mott expects a birth within an hour or two. Otherwise, she’s having trouble.

Calving difficulty—or dystocia—can cause the death of calves and cows, increase the susceptibility of calves to disease,

and lower weaning weights. Cows experiencing dystocia produce less milk and rebreed later than those that give birth more easily. Dystocia costs the U.S. beef and dairy cattle industries more than \$400 million annually.

Heifers are usually bred at 12 to 14 months of age and deliver their first calf at about 2 years. But cows don’t reach their mature size until at least 4 years.

“Breeding them at a young age leads to more calving trouble,” says ARS physiologist Robert A. Bellows. “But the beef and dairy industries depend on producing calves—they can’t afford to support nonbreeding females for 4 years before they get any return.”

For nearly 40 years, LARRL researchers have been helping uncover the causes of calving difficulty and improving the ability of cows to rebreed. Some of their early findings—such as the importance of calf birth weight—have led to industry-wide changes. Now they’re investigating the role of hormones in calving and working to isolate specific genes that would give

SCOTT BAUER (K9490-1)



Herdsmen Jim Watts lifts a calf with a weight scale for a few seconds while Jim Kessler records its birth weight.

cause of calving difficulty: Large calves mean more dystocia. While this finding seems intuitive, previous scientific evidence had been inconclusive.

And larger birth weight is exactly what beef cattle breeders had sought. The weight of a calf when it is weaned at 6 to 8 months determines its market value—and larger birth weights are associated with larger weaning weights.

“But we showed that it’s a trade-off,” Bellows says. “The cost of lost calves and slower rebreeding caused by dystocia diminishes the value of large birth weight.”

Another key, Bellows found, was maximizing growth of the young cows.

“Feeding young heifers so they grow more rapidly from weaning to breeding increases the size of their skeleton and pelvis, which helps reduce dystocia,” he says.

Sires also have a major influence on dystocia, Bellows and colleagues found. “Large, high-gaining sires produce calves with large birth weights,” he says. Sire selection is crucial in balancing desired birth weights and calving difficulty.

Using this information, geneticists developed selection tools to improve calving ease. Additionally, breeders stopped selecting primarily for weaning weight and looked closely at keeping birth weight under control. That helped, but didn’t solve the entire problem.

producers even more breeding tools.

Miles City scientists work exclusively with beef cattle, but because dystocia also affects dairy cows, the dairy industry can apply many of the lab’s findings.

“When I started with ARS in the early 1960s, we knew that dystocia had an economic impact, but there was little information about it,” says Bellows. Now considered an international expert on dystocia, he still consults at the lab, though he retired last year.

Thanks to research by Bellows and others, producers can reduce calf deaths by up to 55 percent and heifer deaths by 80 percent with proper management.

By 1971, Bellows and colleagues pinpointed birth weight as the most important

SCOTT BAUER (K9484-1)



Geneticist Michael MacNeil (left) and physiologist Robert Bellows examine implantable transmitters used to record body temperature and heart rate of cows before, during, and after giving birth.

“When producers apply the research—by selecting sires and cows for reduced calving difficulty and lower birth weights, giving timely obstetrical assistance at calving, and providing proper nutrition before and after calving—the incidence of dystocia decreases up to 25 percent and rebreeding improves up to 15 percent,” says Bellows.

The latest work at the laboratory has been on hormonal and genetic factors influencing dystocia.

“We knew in the 1970s that cows carrying male calves had more difficulty at calving than those carrying females,” Bellows said. “But in 1993, we discovered that it was more than size difference between the genders. Cows carrying male calves have higher testosterone levels than cows carrying females.” That could influence the cow’s ability to deliver a calf, Bellows says.

They’ve also found that cows that have difficulty calving have different estrogen and progesterone levels than cows that don’t need assistance. This may indicate a difference in the degree of relaxation and expansion of the birth canal and the force of labor contractions.

Another project under way: LARRL scientists are working to develop genetic tools that will enable breeders to more precisely select animals having less dystocia.

Ideally, producers want to maximize growth and weaning weight while keeping birth weight low enough to reduce calving problems. The traits are correlated, but researchers have identified a genetic region that may help separate them.

“There are probably many genes that affect those traits jointly,” says ARS geneticist Michael D. MacNeil. “We suspect there are also some genes that act independently, and it appears we’ve found a location on chromosome 2 that influences birth weight

without influencing subsequent growth.”

While the discovery is exciting, it may be a while before scientists determine its value. “We haven’t found the specific gene and don’t know how the region influences birth weight,” he says.

By analogy, MacNeil says the bovine genome is 3,000 units long; in miles, that’s about the distance from New York to Los Angeles. They’ve narrowed the gene location down to a stretch of 30 to 40 units, or to within the Los Angeles metropolitan area in the cross-country analogy.

“It is still a substantial challenge to find the right ‘address,’” says MacNeil.

Mott’s family started selecting sires for lower birth weights years ago, sacrificing some growth but reducing dystocia. In the future, the lab’s work

with hormones and genetics may help ranchers and breeders help their heifers even more.—By **Kathryn Barry Stelljes, ARS.**

This research is part of Food Animal Production, an ARS National Program (#101) described on the World Wide Web at <http://www.nps.ars.usda.gov>.

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A cesarean section may be necessary when calving difficulty is extreme.



SCOTT BAUER (K9479-1)

Where's the Meat?

Animal scientist Alva Mitchell, of the Growth Biology Laboratory at the ARS Beltsville (Maryland) Agricultural Research Center, used dual x-ray absorptiometry (DXA) to measure pork carcass composition. This method is noninvasive and requires little user input in terms of manipulation and data processing. "The technology is based on using x-rays of differing energy levels to scan for soft tissue of differing densities," says Mitchell.

The technology was used in the lab to measure pork carcass composition by performing a total scan of pork carcass halves. Information from selected cross-sections of the image was highly predictive of the composition of the entire carcass.

Hog production has undergone significant changes over the past hundred years. In the first half of the 20th century, market hogs were bred for lard, which was used as a resource during both World Wars. About midway through the century, consumers began looking for leaner meat—highly nutritious but with less fat and calories. The pork industry responded by breeding for leanness. However, it was hard to know just what the lean-to-fat ratio was throughout the carcass without cutting it into its various parts. "Dual x-ray absorptiometry would allow packers to know just what they are paying for: the true value of the meat and not a large amount of fat that gets cut off before shipping," says Mitchell.

Over the years, instrumentation has allowed the fat-to-lean ratio to be determined with an acceptable degree of accuracy.

Now, rapid, accurate methods are needed to provide information regarding the fat and lean content during the on-line processing of pork carcasses.



The DXA instruments Mitchell used scanned cross-sections of the carcass at a

speed of 7.68 centimeters per second, using pencil-beam x-ray technology. This speed compares to the processing chain speed of 16.6 centimeters per second. Newer DXA instruments use a wide-angle or fan-beam technology that will scan wider sections, increasing scanning speed and making the technology potentially adaptable to on-line evaluation of pork carcasses. Mitchell's next step is to find a commercial packing plant to test the technology, which would require adapting it to the processing environment.—By **Sharon Durham**, ARS.

Alva Mitchell is with the USDA-ARS Growth Biology Laboratory, 10300 Baltimore Blvd., Building 200, Room 205, BARC-East, Beltsville, MD 20705-2350; phone (301) 504-8868, fax (301) 504-8623, e-mail mitchell@anri.barc.usda.gov. ★

Foraging Ahead

The U.S. Dairy Forage Research Center, in Madison, Wisconsin, opened its doors in 1981 with a clear vision to assist dairy farmers by increasing the efficiency of forage production and use.

Forages are key crops, both for feeding cows and maintaining sustainable dairy farms. Forage crops provide fiber, energy, protein, vitamins, and minerals to cows and may also be harvested as hay or silage for later feeding.

As a result of the center's research, use of forage crops by dairy farmers is much different today than 20 years ago. Determining forage crop quality is more accurate and rapid. The quality of alfalfa and corn silage, two primary dairy cattle forages, has increased, providing more energy for milk production. Advances in varieties and forage management have reduced the amount of land needed for forage production.

"Over the years, we've learned to listen to our customers and tried to adjust some of our focus in response to their needs," says Neal P. Martin, center director, who assumed leadership in March 1999.

The annual \$11 billion hay crop is the third most valuable crop grown in the United States, after corn and soybeans. So forage crop improvements are paramount to the success of dairy farms.

Over half the forage crops fed to dairy cattle today are perennial legumes and grasses. Beyond their monetary value, grasses and legumes save soil and can be grown on land that's unsuitable for row crops like corn or soybeans. In addition, forages improve water infiltration and are important for managing nutrient problems on dairy farms.

With dairy cows, what goes in affects the quantity and quality of what comes out. That's why intensive studies of dairy cow diets have shown farmers how to balance rations for optimum diets, and that equals better health. A diet with too little fiber and too much concentrate (grains and dietary supplements) is too rich. A diet with too much fiber fills a cow up without providing her enough energy for high milk production. So, center scientists established upper and lower limits of dietary fiber.

Researchers also studied the role of phosphorus in cow diets and its effect on the environment. Excess phosphorus in water runoff from fields can boost algae and aquatic plant growth in streams and lakes. Studies by center scientists showed that feeding dairy cows 20 percent less phosphorus could save U.S. dairy producers \$100 million a year and improve water quality without sacrificing milk production or cow health.

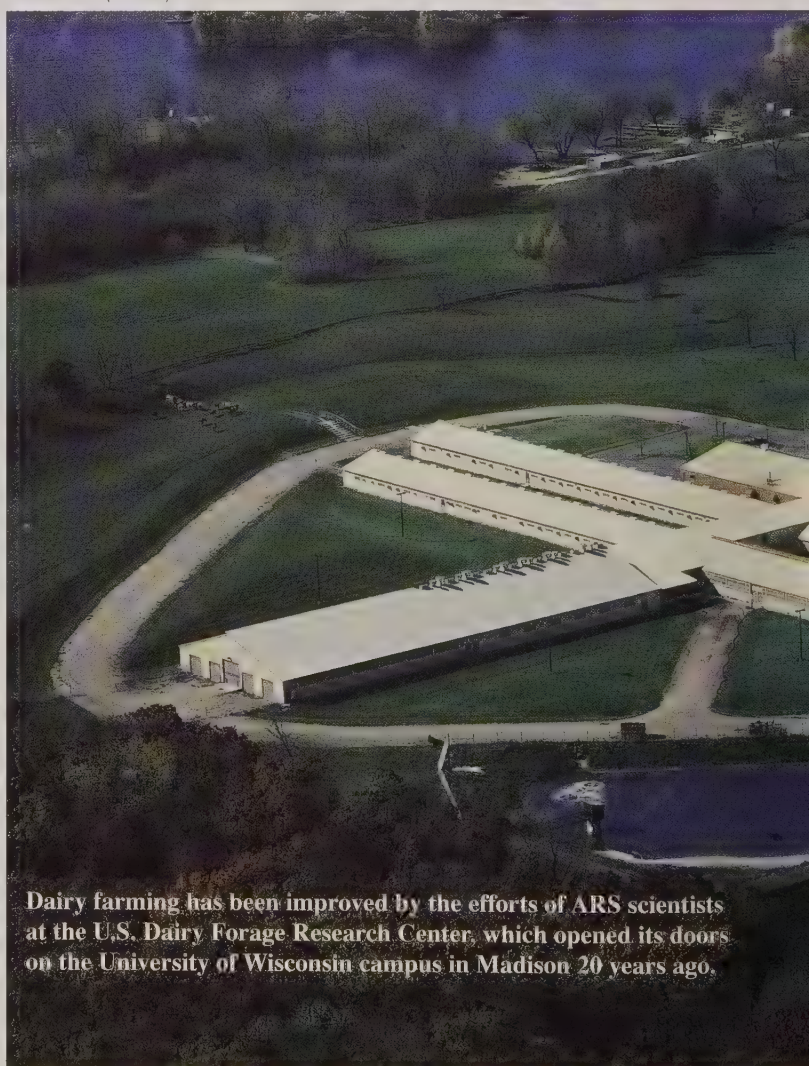
Nitrogen management can also be a problem on dairy farms. The protein in alfalfa silage is broken down into nitrogen

BRUCE FRITZ (K4596-14)



Technician Diane Amundson analyzes concentrates and forages for fiber. Samples are collected weekly, dried, and ground before they are analyzed.

BRUCE FRITZ (K1100-6)



Dairy farming has been improved by the efforts of ARS scientists at the U.S. Dairy Forage Research Center, which opened its doors on the University of Wisconsin campus in Madison 20 years ago.

Research Highlights From the U.S. Dairy Forage Research Center

- Determined that proper roasting of soybeans for dairy cow diets generates \$20 to \$40 million annually in added value.

- Developed a field macerator that reduces alfalfa hay drying time by 2 days, increases dry matter digestibility, and improves protein use by the cow.

- Developed a dairy forage systems model (DAFOSYM) to evaluate alternatives for forage crop production, harvest, storage, and feeding, while measuring milk and manure production.

- Increased persistence, longevity, yields, and disease resistance of red clover varieties, leading to annual savings of \$140 per acre.

- Gained a better understanding of lignin chemistry and phenolic-carbohydrate cross-linking, which affect digestibility of cell walls.

- Developed a method to screen feeds for rumen-undegradable protein and for optimizing feed pre-treatments to enhance rumen-undegradable protein.

- Demonstrated that alfalfa can be highly effective for cleaning up nitrate-contaminated sites.

- Determined the relative value of various feed proteins as supplements for lactating dairy cows fed alfalfa silage as their principal forage.



compounds, which the cow does not use efficiently. Center scientists are investigating ways to preserve protein during ensiling and improve nitrogen use by the dairy cow.

Farmers have several good reasons for growing alfalfa. It fixes nitrogen, meaning there's no need to add nitrogen fertilizer, and it's the best scavenger of excessive soil nitrate left by overfertilized row crops, thus saving money and abating potential environmental problems.

Scientists at the center are helping dairy farmers by developing value-added products from alfalfa and other perennial legumes. Alfalfa fiber can be used to make lactic acid, a precursor to biodegradable plastic. Genetically modified alfalfa has been used to produce high-value enzymes like phytase, which helps pigs and chickens use phosphorus in their diets more efficiently.

Producing quality products from agricultural crops without depleting our land is the cornerstone of sustainable agriculture for all farmers—big and small.

"Sustainable agriculture helps farmers put more money in their pockets and less into production costs for fertilizers and pesticides," says Martin.

Yet another way the Dairy Forage Research Center's research has responded to customer needs is development of a simple graphical method whereby farmers can decide whether to apply bacterial inoculants before ensiling. Bacterial inoculants are the principal silage additives in the United States. They supply extra lactic acid bacteria to the crop to ensure fast and efficient fermentation in the silo. The system uses weather and harvest information to predict when an inoculant will be successful and was tested on farms in Wisconsin and New York.

This research, coupled with lactation studies at the center, showed how much milk-production response could be achieved with silage inoculants. The studies provided the first logical basis for helping farmers know when bacterial inoculants can be used profitably in making alfalfa silage. About 50 million wet tons of alfalfa are ensiled annually in the United States, and 30–50 percent of this tonnage is inoculated at a cost of about \$1 per ton.—By **Linda McGraw**, ARS.

This research is part of Food Animal Production (#101), Rangeland, Pasture, and Forages (#205), and Integrated Agricultural Systems (#207), three ARS National Programs described on the World Wide Web at <http://www.nps.ars.usda.gov>.

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Detecting Stress in Animals

When people get stressed, they seek relief in many ways. Some exercise, some practice specific breathing techniques, and some eat chocolate. Farm animals become stressed, too. In domesticated food animals, stress can affect meat quality, milk production, and general health. But animal stress must often be intuited from clues such as lower-than-anticipated weights and increased illness.

Certain stressful events can be anticipated, for example, birth and weaning. But how do you know if an animal is stressed for some other reason? Ted H. Elsasser of ARS' Growth Biology Laboratory in Beltsville, Maryland, is investigating nitrated protein as a biomarker of stress. Nitrated proteins may serve as an early-warning system to point out an animal that may yield unsafe products or flag a need for therapeutic or intervention strategies to promote recovery from illness.

"The biggest problem for animal producers is disease management, so an early warning system would certainly be helpful," says Elsasser.

Other researchers have found that nitrated proteins are formed when certain components of proteins—tyrosines—become nitrated along critical parts of the regulatory pathway, altering the function of the proteins. This occurs after high levels of infectious stress, injury, or the presence of immune system hormones called inflammatory cytokines.

These changes in proteins occur in humans and other animals. But all nitrated proteins are not the same. Specific protein nitrations are associated with specific disorders, depending on the protein altered and the position of the alteration on the protein. Proteins are like jigsaw puzzle pieces that are designed to fit together. When proteins are altered, they no longer fit with other proteins, and they become ineffective. Different stresses are reflected in different biochemical systems of the body—resulting in different

patterns and profiles of nitrated proteins. To complicate matters more, not all animals' biochemical pathways respond to the same stresses in the same way.

The protein nitrification process begins with arginine, an amino acid that is present in the diet and circulates in the bloodstream. If significant stress is present, more arginine is transported into cells by a specific transporter. This is one of the body's initial attempts to fight harmful consequences of stress.

Various biochemical pathways cause nitric oxide to be generated from the arginine. Depending on how cells have responded to stresses, their internal oxidative environment can change. Under some circumstances, the nitric oxide reacts with oxygen, creating a compound called peroxynitrite. It is this peroxynitrite that reacts with amino acids in proteins, tyrosines in particular, to form a nitrated protein.

Antioxidant compounds can control some of the processes through which peroxynitrite is formed. Just as we get vaccinations before foreign travel to ward off illness, Elsasser is investigating the possibility of preconditioning animals with antioxidants before predicted stresses to head off subsequent illness. Just as they mop up free radicals in the body, antioxidants combat some of the chemical reactions in cells that result in nitrated protein formation. It is important to note that nitrated proteins are not the same as free radicals.

Stress causes several undesirable effects, including slow animal growth and lowered immune response.

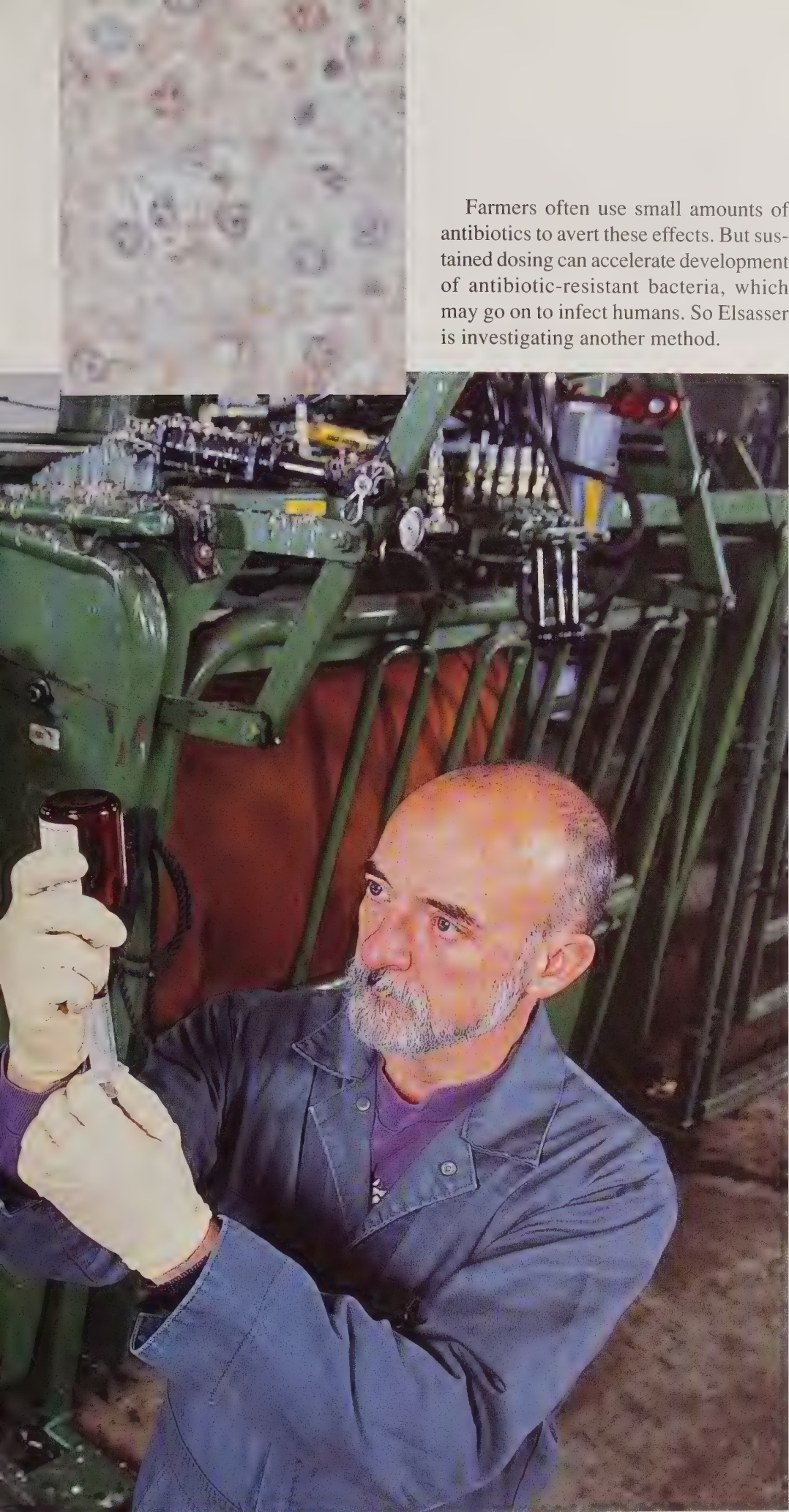
Above left: Normal liver cells.

Middle: The reddish-brown color indicates presence of nitrated proteins that developed in response to stress from bacterial toxin.

Right: Pretreatment with vitamin E appears to limit development of nitrated proteins.

Animal scientist Ted Elsasser prepares an injection of vitamin E to test its ability to relieve some effects of bacterial toxins.

SCOTT BAUER (K9759-1)



Farmers often use small amounts of antibiotics to avert these effects. But sustained dosing can accelerate development of antibiotic-resistant bacteria, which may go on to infect humans. So Elsasser is investigating another method.

An Alternative Approach

Enter vitamin E, a standard antioxidant supplement in many people's nutritional regimen. "Our studies using vitamin E as a weapon against animal stress may offer some relief," says Elsasser. He gave six calves vitamin E as a pretreatment before challenging them with a toxin taken from bacterial cell walls. This toxin causes the immune system to react as if an infection were present. Elsasser also gave six calves only the toxin, and four received neither the toxin nor the vitamin E.

Compared to the four untreated calves, all the calves challenged with the toxin had significantly lower concentrations of IGF-I, a metabolic growth factor, in the liver and blood. However, those calves that were injected with toxin and pretreated with vitamin E had higher IGF-I concentrations than the calves that received only the toxin. The cattle given vitamin E also recovered more quickly from the systemic effects of the toxin. Pretreating with vitamin E could have significant benefits.

"Using vitamin E as a preconditioner allows us to maintain growth rates better and perhaps prevent secondary infections, which crop up when stress creates an opportunity for a pathogen to gain a competitive foothold," says Elsasser. Being able to prevent infections due to stress could lead to lower disease-management costs, less antibiotic use, and healthier animals. And healthier animals mean that fewer disease-causing microbes make their way to human consumers.—By **Sharon Durham**, ARS.

This research is part of Food Animal Production, an ARS National Program (#101) described on the World Wide Web at <http://www.nps.ars.usda.gov>.

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Worldwide Effort To Map the **Bovine Genome**

KEITH WELLER (K9977-1)



Molecular biology technician Renee Godtel prepares bovine DNA samples for sequencing.

First there was the mapping of the human genome. Then, this spring, scientists announced they had nearly completed the genome mapping of the mouse. Now, scientists are in the early stages of mapping the bovine genome to help produce cattle with improved production traits and to possibly help in finding cures for human diseases.

The Agricultural Research Service is part of a group of government and university laboratories from four continents in the initial stages of mapping the bovine genome. The ARS research effort is led by Steven Kappes and John Keele of the Roman L. Hruska U.S. Meat Animal Research Center, in Clay Center, Nebraska. Kappes is center director, and Keele is an animal scientist.

The project began in spring 2000, when Kappes started contacting labs from around the world to develop a physical (bacterial artificial chromosome—BAC) map of cattle. Bacteria—and more specifically, bacterial chromosomes—are used as hosts for pieces of bovine chromosomes. The bacterial hosts are used to generate many identical copies of a piece, or clone, of cattle DNA. The BAC map will be a useful tool for identifying genes that affect production traits in farm animals and an excellent resource to improve the efficiency of a future effort to sequence the entire bovine genome.

The first step in the process is to fingerprint individual BAC clones. Researchers at the British Columbia Cancer Agency Genome Sciences Centre have been funded to construct a fingerprinted BAC map. A fingerprint is obtained by cutting DNA from a BAC clone into pieces and separating the fragments on a gel. The fingerprint pattern of the different fragments is used to identify overlapping BAC clones. A BAC map is the collection of overlapping clones that represent the entire bovine genome.

Funding for this part of the project has been provided by USDA-ARS; the Biotechnology and Biological Sciences Research Council and Roslin Institute, from the United Kingdom; the University of Alberta and the Alberta Science and Research Authority, in Canada; and the University of Illinois.

The fingerprinting will be performed on 280,000 BAC clones from two libraries constructed by scientists at the Children's Hospital Oakland (California) Research Institute. The first BAC library was constructed from Holstein bull DNA and the second from Hereford bull DNA. Each BAC clone contains about 170,000 bases of cattle DNA.

The second step, which can occur simultaneously with fingerprinting, is sequencing both ends of all 280,000 clones. This work is being conducted by ARS, the University of Illinois, Texas A&M University, AgResearch of New Zealand, the Commonwealth Scientific and Industrial Research Organization of Australia, the Brazilian Agricultural Research Corporation, and the University of Alberta. The Institute of Genomic Research in Rockville, Maryland, has been contracted to do some of the sequencing. The National Institute for Agricultural Research in France is fingerprinting and end-sequencing clones

from a BAC library constructed in their laboratory. They will combine their information later with the international effort. Kappes is talking with other organizations to help with the end sequencing.

The scientists will combine the end-sequencing and fingerprinting information to determine the overlapping BAC clones. Kappes says, "Ideally, we would like one set of contiguous overlapping clones—'contigs'—for each of the 30 chromosomes in the bovine genome. But it's likely that we'll have gaps between several contigs for each chromosome."

So far, 249,000 of the 280,000 cattle BAC clones have been fingerprinted, and the end-sequencing effort is under way. The completion date for the bovine BAC map is February 2003.

The researchers hope that the next phase of the project will be sequencing the bovine genome. Kappes and other scientists have sent a proposal to the National Institutes of Health (NIH) to do this work.

The BAC map alone costs \$4.5 million, while NIH estimates it may cost \$100 million to sequence the bovine genome to a finished stage. Kappes says the effort is expensive, but it will have many tangible benefits. Scientists from ARS and elsewhere will use the BAC map and sequence information to improve productivity traits in cattle. This means they may be able to more accurately select genetically superior animals for specific needs, such as lean beef, milk production, reduced feed requirements, and improved health and welfare. This ability would increase the profitability of beef production. The research should also benefit those who raise sheep, since the genetic makeup of sheep is very similar to that of cattle.

This research may also help the medical community. "As we define certain biological mechanisms in livestock, the information may benefit human medicine," says Kappes. "We are currently defining a genetic mechanism affecting muscling in sheep. This is of specific interest to research efforts in human medicine because a similar mechanism is observed in cancer cells."

Not only is there similarity in the DNA sequences of genes in farm animals and in humans, but also the biological processes are very similar across species. Eventually, researchers will be able to compare the human genome to the bovine genome to help determine the function of genes for both livestock production and human well-being.—By **David Elstein**, ARS.

This research is part of Food Animal Production, an ARS National Program (#101) described on the World Wide Web at <http://www.nps.ars.usda.gov>.

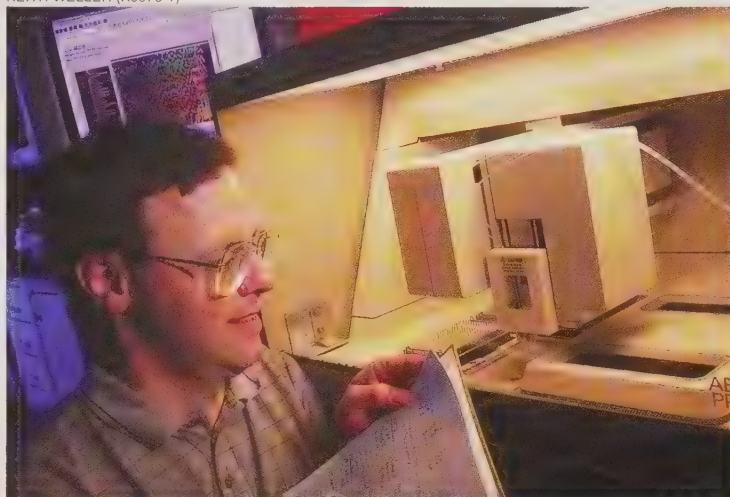
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KEITH WELLER (K9978-1)



Along with the genomics group at MARC, animal scientist John Keele is part of the team that's working to produce a BAC map of the bovine genome.

KEITH WELLER (K9976-1)



Chemist Tim Smith observes an automated DNA sequence instrument, which produces 96 bovine DNA sequences every 3 hours.

DUANE SMAILUS (K9976-20)



At the British Columbia Cancer Agency Genome Sciences Center in Vancouver, Canada, genomics technologist Pawan Pandoh prepares BAC fingerprints used in creating the bovine map.

Can Egg Follicle Size Indicate Cow Fertility?

According to Tom Geary—a reproductive physiologist at ARS' Fort Keogh Livestock and Range Research Laboratory in Miles City, Montana—only two out of three beef cows that are bred actually give birth. Identifying the most fertile cows could help producers achieve higher pregnancy rates in their herds and make their operations more efficient.

For several years, Geary has been collaborating with professor Michael F. Smith, a reproductive physiologist at the University of Missouri-Columbia. They have been looking for different physiological indicators of fertility in beef cows.

Now, George Perry—a graduate student of Smith's who's been working with Geary—may have discovered a new indicator of beef cow fertility, at least in some situations: the size of egg-bearing structures called follicles. Their studies may ultimately benefit producers who would like to artificially inseminate all

their beef cows at the same time and rapidly improve the genetics of their herds.

Inside the Cow's Reproductive System

A beef cow has a 21-day estrous cycle, the period from one estrus, or heat, to the next. The estrous cycle is largely controlled by structures called follicles on the cow's ovaries and the hormones these structures produce.

As a cow approaches estrus, a follicle containing an oocyte (egg) appears like a blister on an ovary. The follicle contains cells that produce estrogen. As the follicle grows, the estrogen eventually reaches a threshold level that causes the cow to be in heat. Shortly thereafter, the cow ovulates: the follicle ruptures and releases the egg into the uterus. Later, another hormone—progesterone—is produced. It prepares the uterus for pregnancy and helps maintain the pregnancy.

Geary says, "Many research projects have been conducted in which natural hormones are administered to beef cows

to synchronize ovulation. But cows that are artificially inseminated after induced ovulation seem less fertile than cows inseminated after a natural heat."

As part of his doctoral research, Perry wanted to figure out why this decrease in fertility occurs. Earlier studies had shown that when dairy cows are induced to ovulate, they exhibit a wide range of follicle sizes. Perry says, "We hypothesized that the synchronized beef cows would also ovulate a wide range of follicle sizes. This could affect estrogen and progesterone levels—and fertility."

To test this hypothesis, the researchers studied 45 cows at the University of Missouri in 2001. Perry measured their ovulating follicles when they were induced to ovulate, but before artificial insemination. Using an ultrasound machine, he classified each cow's ovulatory follicle as small (less than 12 millimeters), medium (12.5–16 mm), or large (more than 16 mm). About 4 weeks after the cows were inseminated, he used

PEGGY GREB (K10360-1)



Reproductive physiologist Tom Geary prepares to take a blood sample from a cow to measure her hormones. An ultrasound monitor on the right indicates this cow is 45 days pregnant.



PEGGY GREB (K10364-1)

Technician George Perry conducts a radioimmunoassay to measure progesterone concentration in serum samples from cows that ovulated different-sized follicles.

ultrasound to determine whether they were pregnant.

The scientists found that 25 days after breeding, only about 57 percent of the cows with small follicles were pregnant, and by day 60, only 29 percent were still pregnant. Of the cows with large follicles, however, 67 percent were pregnant at day 25, and they all remained pregnant through day 60. Even more impressively, 78 percent of the cows with medium follicles were pregnant at day 25, and 71 percent were still pregnant at day 60.

These results convinced the scientists to repeat the study on a larger scale. In 2002, they began research on 273 cows at the Fort Keogh lab. Although the study had grown considerably, they noticed the same general trend of small-follicle cows having lower fertility.

Because there were more animals, the researchers could compare more specific follicle size groups. All embryonic deaths occurred in the synchronized cows with ovulatory follicles less than or equal to 11 mm.

Though their data reiterated the importance of follicle size, the scientists determined something else during the Fort Keogh study. Cows that expressed a natural heat also had ovulatory follicles

of varying sizes. But regardless of whether the follicles were small, medium, or large, the cows' fertility rates were similar.

Natural Heat vs. Induced Ovulation

Cows in heat allow other cows to mount them, showing producers when to breed them. However, heat detection is unnecessary in cows that are induced to ovulate at a specific time.

Although the cows in the Fort Keogh study were all supposed to ovulate at the same time, not all did. To detect those that came into heat naturally, the researchers outfitted the entire herd with electronic transmitters. Geary explains, "The transmitters are glued to the tail-head of the cows and allow us to continuously monitor for mount activity. A computer records the time and duration of each mount."

Adds Perry, "We considered a cow to be in standing estrus, or heat, when she received three mounts lasting 2 seconds or longer within a 4-hour period." At that point, the researchers measured her follicle size.

The follicle sizes of the cows that exhibited a natural heat varied just as much as those of cows induced to ovulate. However, it appears that if the follicle is capable of ovulating naturally, it doesn't matter what size it is. A cow in standing estrus with an 11-mm follicle has the same chance of becoming pregnant and maintaining the pregnancy as a cow with a 16-mm follicle. Follicle size seems to affect fertility only if cows are induced to ovulate.

The Bigger Picture

Although follicle size isn't quite the fertility indicator the researchers thought, the information they gathered may still benefit U.S. beef producers and help them manage herds more efficiently.

Geary explains, "Currently, less than 6 percent of U.S. beef cows are artificially inseminated because of the cost associated with detecting when a cow is

in heat. But scientists in industry and academia continue to look for more effective ways of inducing ovulation, so producers won't need to dedicate valuable resources to heat detection."

"Our follicle research will help us focus on where problems are occurring with current estrus synchronization and artificial insemination protocols," adds Perry.

Ultimately, such protocols will allow cattle producers to inseminate a large number of animals at once with genetically superior germplasm and simplify the management of pregnant animals.—
By **Amy Spillman**, formerly with ARS.

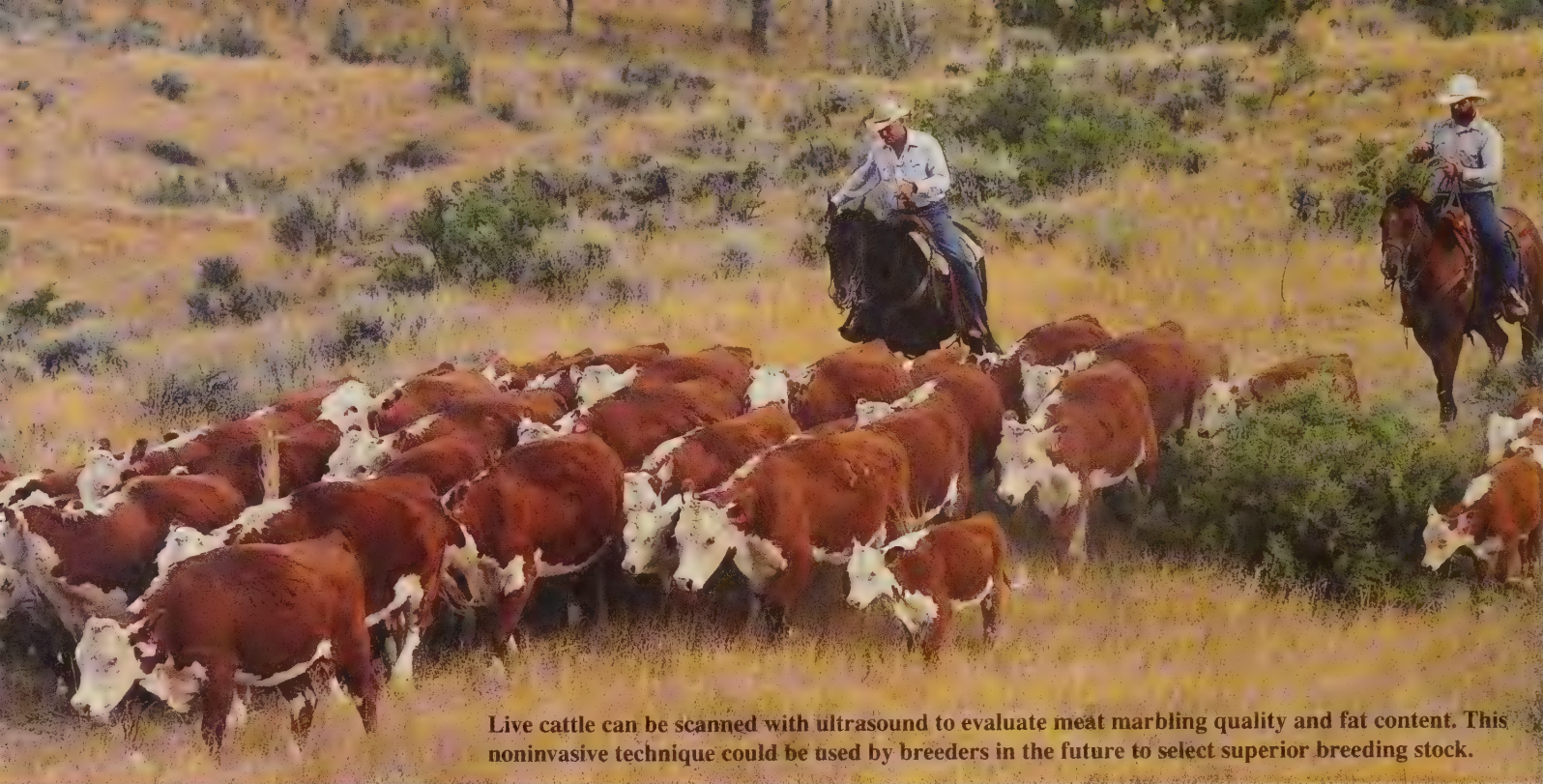
This research is part of Food Animal Production, an ARS National Program (#101) described on the World Wide Web at www.nps.ars.usda.gov.

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PEGGY GREB (K10366-2)

Three-year-old cow with newborn calf. Natural or induced ovulation of a large follicle results in normal fertility and the birth of a live calf.



Live cattle can be scanned with ultrasound to evaluate meat marbling quality and fat content. This noninvasive technique could be used by breeders in the future to select superior breeding stock.

JACK DYKINGA (K3908-15)

Ultrasound Helps Producers Find Ideal Cattle

Ultrasound is commonly used by doctors to check on the health of a human fetus or to scan a patient's organs. Ultrasound has also been used to study fetuses in livestock. But now, Agricultural Research Service and Iowa State University scientists have found that scanning a live cow with ultrasound can determine its fat and marbling qualities just as well as measurements taken on the carcass can.

Ultrasound is delivered via a small, noninvasive, hand-held probe that emits sound waves. These sound waves are turned into images that are displayed on a monitor so researchers can see inside the body. Trained technicians use the same machine as obstetricians do, but it has been modified for livestock use. The probe is placed on the animal's back (the

part used in rib-eye steak) to see how lean and muscular the animal is as well as how much marbling it has. Marbling—the little pieces of fat in the middle of steaks—adds flavor.

The research on using ultrasound to determine carcass quality was conducted cooperatively by Iowa State University and ARS scientists using steers produced and evaluated at ARS' Roman L. Hruska U.S. Meat Animal Research Center (MARC) in Clay Center, Nebraska. Ultrasound evaluations and data analyses were conducted by Scott Greiner, now an extension agent at Virginia Tech University, at Iowa State University in the early 1990s. But researchers have been using ultrasound on livestock since the 1950s. Producers want ways to know whether the cattle they breed will produce quality beef, but they usually know this only when the animal has been processed.

While scanning each animal may take only a few minutes, research leader Larry V. Cundiff says this technology will be used mainly by producers of breeding

stock. "It can be used to identify and select superior breeding stock for production of progeny with high levels of marbling and relatively low levels of fat trim," Cundiff says.

The researchers at MARC and Iowa State developed equations to see how accurate ultrasound is in determining quality beef. Greiner states, "With ultrasound, the predicted composition of the live animal closely matches the composition seen in the carcass."

The Angus breed of cattle is the most popular one on which to use the technology, but ultrasound can be used on all breeds. "The industry has widely and rapidly adopted ultrasound use," Greiner says. Each ultrasound—which includes the machine, probe, computer hardware and software, and other supplies—costs between \$20,000 and \$25,000, he says.—By **David Elstein, ARS.**

This research is part of Food Animal Production, an ARS National Program (#101) described on the World Wide Web at www.nps.ars.usda.gov.

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No Wool? No Problem!

A thick coat of wool is one of the most recognizable features of sheep. Even when seeing a sheep that has been recently sheared, we know that the wool will soon reappear. But what if there were sheep that had no wool at all—but instead, hair that is similar to humans’?

Believe it or not, there are a few breeds of sheep raised in the United States that have just that. Some of these breeds have been around for more than 50 years. Now Agricultural Research Service scientists are determining through genetics which breeds should be mated to produce “easy-care” sheep. Work on this sheep breeding project began in 2000 and is led by geneticist Kreg A. Leymaster of the Roman L. Hruska U.S. Meat Animal Research Center (MARC) in Clay Center, Nebraska.

According to Leymaster, the price of wool has been going down. Consequently, the cost of shearing a sheep sometimes exceeds the price at which the wool can be sold. On the other hand, demand for the meat of sheep—especially within certain ethnic groups—is increasing dramatically, and U.S. producers cannot keep up. Many of the chops and other lamb cuts in our markets actually come from Australia and New Zealand. ARS is conducting research to help U.S. ranchers become more competitive in selling sheep for food.

“The U.S. sheep industry encouraged evaluation of hair breeds as a possible

means to increase profits for ranchers,” Leymaster says. So now he is investigating which combination of sheep—using both wool and hair breeds—would be best for farmers and consumers alike. Sheep with hair don’t need to be sheared, and that means lower labor costs.

Leymaster bred rams of four breeds. He used two hair breeds (Katahdin, which was developed in the 1950s in Maine; and Dorper, which was brought to the United States from South Africa 7 years ago) and two wool breeds (Rambouillet and Dorset). He mated the four breeds to 360 Romanov ewes in 2000, 2001, and 2002. Romanov sheep are known for their early sexual maturity, and they produce more lambs than other breeds. Leymaster is trying to find the combination of breeds that can produce meat most efficiently.

This study is the first to directly compare the two hair breeds, and there is only

limited information on hair breeds in general, Leymaster says. Both Dorper and Rambouillet have evolved under extensively dry conditions, while Dorset and Katahdin have been bred in more favorable environments.

The research should help U.S. ranchers find the most profitable and efficient breed of sheep for their farm type. Leymaster hopes to evaluate 300 crossbred ewes of each breed through the 3 years of mating.—By **David Elstein**, ARS.

This research is part of Food Animal Production, an ARS National Program (#101) described on the World Wide Web at www.nps.ars.usda.gov.

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KREG LEYMASTER (K10379-1)



Sheep that produce hair (like this Dorper ram, in the foreground) instead of wool don’t need shearing, an expensive, labor-intensive process. Elimination of shearing may increase profits for producers interested in producing meat rather than wool. Behind the Dorper ram in the photo is a Romanov ewe.

Well-Rounded Bulls Bring Profit to Cattle Breeders

For years, beef cattle producers have kept track of characteristics of their animals to selectively breed them and improve specific traits, such as growth rate, fat content, or marbling. Unfortunately, selectively breeding to improve one characteristic can lead to undesirable correlated responses, such as reproductive inefficiencies.

Now, geneticists Michael MacNeil, at ARS' Fort Keogh Livestock and Range Research Laboratory in Miles City, Montana, and William Herring, his industry collaborator, have helped producers move beyond simply breeding to improve individual traits. The researchers have set up a program that helps evaluate and rank animals based on multiple traits and select those that have the potential to produce the most profitable offspring.

In the beef cattle industry, breeders record growth traits such as weights at birth, weaning, yearling, and maturity;

carcass traits such as lean yield, marbling, and fat content; and reproductive traits such as the age when a female reaches puberty and whether she becomes pregnant each year.

Breed associations take this information, combine it with each animal's genetic tree, and calculate expected progeny differences, or EPDs. The EPDs give producers an estimate of how the future progeny of one animal will compare to those of another animal within the breed, for a specific trait. By comparing EPDs, for example, they would be able to determine that bull A is more likely to produce offspring with greater marbling than bull B.

Breeding for Profit: A Balancing Act

"Until now, producers have been left with the difficult task of combining these EPDs efficiently," says Herring. "They have had to decide whether growth rate is more important than marbling or

whether yield grade is more important than weaning weight."

But MacNeil has designed software that estimates the relative economic value of each trait in a stereotypical production system. This information, combined with an animal's EPD data, can be used to estimate that animal's overall genetic profit potential.

Since 1996, Herring has worked with the Angus Sire Alliance and Circle A Angus Ranch in Missouri to rank sires nominated by Angus breeders throughout the United States by their genetic profit potential, using relative economic values that he and MacNeil calculated.

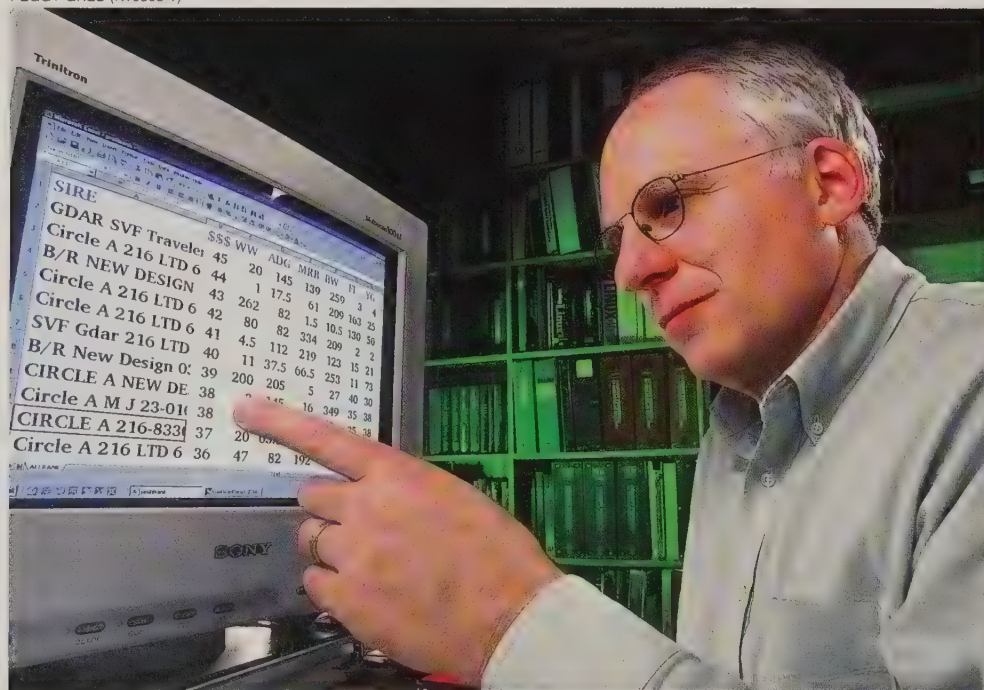
Commercial Angus females at Circle A locations in Huntsville, Iberia, and Stockton, Missouri, are randomly mated to Angus test candidates and reference sires. Data on progeny are then collected, including their birth weight, weaning weight, postweaning daily gain, daily dry-matter intake, marbling score, and yield grade.

The researchers use MacNeil's bio-economic modeling software to calculate sire rankings. They have found that among the 352 sires tested so far, there exists a range in profitability of \$41.65. This means that if the highest and lowest ranking bulls were used in a production system similar to the one described in the economic simulation, a difference in profitability of more than \$40 per progeny would be expected.

MacNeil says, "There is no single trait that ensures a bull's offspring will be highly profitable." For example, the marbling rankings of the top five bulls overall range from 1 to 334, and their rankings for yield grade range from 1 to 50. For the other traits, the variability in rank is similar.

ABS Global Inc., based in De Forest, Wisconsin, has leased eight of the top-rated bulls from the Angus Sire Alliance. Doug Frank, an ABS manager, says, "We've been following the alliance since its inception in 1996. We were intrigued by the way data on the animals was being

PEGGY GREB (K10368-1)



Geneticist Michael MacNeil examines results from genetic analysis of sires used in the Angus Sire Alliance program at Circle A Angus Ranch. Economic values for individual traits are used to sort bulls by potential profitability of their offspring. These values are products of ARS research led by MacNeil.

compiled and negotiated the right to lease the top two bulls every year. Testing them takes about 2 years to complete.”

In marketing the bulls, ABS publishes their overall profitability EPDs. During an 18-month period between 2001 and 2002, the company sold 75,000 units of the bulls’ semen, which was worth more than \$1.5 million in retail revenue.

“The alliance bulls are popular because of their multitrait performance,” says Frank. “Two of them have been among our top 10 bulls in terms of semen sales.”

Based on the results of this research, MacNeil believes that wide differences exist in the profit potential of cattle. He says that producers should be encouraged

to use a more comprehensive and objective approach than single-trait selection in choosing how to breed their animals. Bulls that have a desirable balance of traits may, in the end, be much more profitable than those that excel in just one or two traits.—By **Amy Spillman**, formerly with ARS.

This research is part of Food Animal Production, an ARS National Program (#101) described on the World Wide Web at www.nps.ars.usda.gov.

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PEGGY GREB (K10377-1)



Above: Line 1 Hereford bulls enjoy fresh silage on a cold day. These bulls will sire a future generation of calves for seedstock and commercial breeders nationwide.



Left: This bull, called New Design 9150, is one of the top-ranked bulls for producing profitable progeny in the Angus Sire Alliance. The high rating results from a combination of traits, including outstanding calving ease and overall carcass merit.

Precise Feed Measurement's a Useful Tool

During the fall of 1998, the Circle A Angus Ranch in Huntsville, Missouri, installed a system that allows ranch managers to measure the daily individual feed intake of steers. This system is similar to those in place at research laboratories like ARS’ Fort Keogh Livestock and Range Research Laboratory.

Twice a day, a computerized wagon doles out a precise amount of feed into gated bins. Each steer is outfitted with a collar holding a computer chip. When the steer approaches its assigned bin, the chip triggers the gate to open so it can eat; the

door closes when the steer walks away. Later, the wagon vacuums up the leftovers and records these amounts.

While geneticist William Herring was working at the University of Florida’s North Florida Research and Education Center, the ranchers sent feed intake data and other measurements to him for analysis. Herring measured feed-conversion rates ranging from 4.3 to 8.9 pounds of dry matter intake per pound of gain. Herring is now with NPD (USA) Smithfield Foods, in Roanoke Rapids, North Carolina.

Geneticist Mike MacNeil, of the Fort Keogh laboratory, says, “Improving feed efficiency could help ranchers increase their profits through reduced input costs. This is clearly one of the traits that should be taken into account in evaluating the genetic profit potential of bulls.”

Grass-Fed Cattle Follow the Appalachian Trail

A major project is under way to design year-round grazing systems for pasture-raised beef in the Appalachian Mountains and the Southeast. More than 20 scientists are involved, including animal nutritionists and behaviorists, meat scientists, agronomists, extension agents, veterinarians, economists, plant physiologists, and soil scientists.

Although some U.S. farmers already raise grass-fed beef, “Our ultimate goals are to extend the grazing season to year-round and produce a consistently high-quality product,” says James P. S. Neel. He’s an animal scientist at the ARS Farming Systems Laboratory in Beaver, West Virginia. “A year-round grazing season would ensure that fresh beef is available throughout the year.

“This could also be done by having grass-fed herds from north to south throughout the Appalachian region. That would take advantage of southern winters, which are mild, and avoid the problems of hot-weather pastures,” Neel says.

The Appalachian area has mostly small family farms on which calves are raised, typically on 50 to 500 acres of woods and pasture. The land is generally too steep to plant crops, so grazing livestock is common. But these farms have trouble competing with larger, highly mechanized farms for the beef

market. Research leader William M. Clapham and others at the Beaver lab thought that these farms might do better aiming for the grass-fed, “natural” beef niche, directly marketing the beef to retail outlets and grocery suppliers.

Cattle would graze Appalachian pastures intensively and be rotated from paddock to paddock, just as grass-fed Argentine cattle graze on the South American pampas. The Argentine niche product commands a premium price in specialty food markets and is currently supplied to American restaurants, supermarkets, and health food stores. Appalachian beef could capture some of this market and increase the net income of the farmers in the Appalachian area.

An Ambitious Joint Endeavor

This project is running the gamut of beef production and marketing—from birth to plate. It’s broad in scope and is a collaboration of four institutions in three states. Working with the ARS scientists in Beaver are colleagues at the Virginia Polytechnic Institute and State University (Virginia Tech), West Virginia University (WVU), and the University of Georgia (UGA). This collaboration is unique because resources are pooled, and each phase of the production stream is assigned to a different institution. Virginia Tech is responsible for the cow/

PEGGY GREB (K10994-2)





Jim Neel uses ultrasound on finishing steers at Willow Bend, West Virginia, to estimate back fat, rib eye area, and intramuscular marbling, all indicators of meat quality.



At the Virginia Tech Shenandoah Valley Agricultural Research and Extension Center, technician Marnie Caldwell (left) and farm manager Dave Cuddy record plate meter measurements, which are used to estimate forage yields in cow-calf grazing paddocks.

calf operation from birth to weaning, preparing the cattle for wintering or market, and conducting the feedlot control at Steele's Tavern, Virginia, near Staunton. WVU is responsible for heifer development and the winter stocker phase in Morgantown, West Virginia. ARS is responsible for pasture finishing at Willow Bend, West Virginia, and overall project management. UGA, in Athens, Georgia, is responsible for meat analysis and conducting a taste panel.

The first 4 years of the project are for testing various production techniques through three calf-to-market cycles. Then the scientists will use on-farm pilot projects to transfer successful techniques to farmers in the central Appalachian Mountain region. "Actually," says Neel, "we're giving out information to farmers as we go. Each institution has designed different pasture systems to meet farmer goals while minimizing possible financial harm from drought and other risks."

Researchers focus on the three aspects of pasture management that farmers have control over: fertilizing and conditioning soil, establishing and managing pastures, and grazing livestock. They're also testing varying levels of fertilizers, measuring everything from grass growth to environmental influence and checking the quality of both the soil and pasture grasses. They assess the risks associated with different production strategies and the likely level of consumer interest in the product.

Methods are surprisingly high-tech, like using near-infrared reflectance spectroscopy to determine pasture quality and ultrasound to measure body composition changes from winter through the finishing period. Computer models correlate various factors—such as animal health, forage quality, and weather—with deviations from target gains. Clapham modeled growth and development of several forages and designed the pasture systems for WVU's farm in Willow Bend. This system took into account environmental extremes and lowered risks associated with weather.

In spring 2001, the first calves were born at Willow Bend and at the Steele's Tavern farm. They were weaned and then sent to Morgantown in early December for winter-feeding treatments. In April 2002, half the steers were sent to a feedlot in Steele's Tavern, while the rest stayed in West Virginia to graze rotationally.

"Pasture-finished animals were fed only high-quality forage at all times—as much as they wanted," says Neel. The feedlot cattle were finished the traditional way—on corn, corn silage, and protein/mineral supplements. All cattle go to market in the fall of each project year. A rib section from each steer is sent to UGA for meat-quality analysis.

"The meat is leaner than feedlot beef, having half the saturated fat and more of the good types of fat. And it's been as tender and tasty as feedlot beef," Clapham says.

Weight Gain and Meat Quality

Researchers are scrutinizing the effects of different winter weight gains on meat quality to determine exactly how much gain is really optimal. "That knowledge will not only help grass-fed-cattle operations, but also feedlots," says Neel. "We believe that a minimum three-quarter pound gain per day is needed, with steers weighing 650 to 700 pounds after winter. But there's little science to back up those recommendations. Most are based on economics, not quality of the end product."

"We're raising these animals for customers who prefer that their beef come from cattle that consume the food they're uniquely designed to eat—grass and forage plants," says Neel. "We try to keep everything as natural as possible. By not finishing animals in a feedlot, there are no feedlot-related illnesses, and so there's less need for medications. We don't give the grass-fed cattle any antibiotics unless they become sick."

Clapham supervises the entire project, which involves a lot of organizing, scheduling, and managing. It is like a virtual ARS location. "We're unique because we have so many disciplines and locations all working as one team to bring each herd from birth to market," he says.—By **Don Comis**, ARS.

This research is part of Rangeland, Pasture, and Forages (#205) and Food Animal Production (#101), two ARS National Programs described on the World Wide Web at www.nps.ars.usda.gov.

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Can You Have Your

Beef and Eat It Too?

*ARS research
brings healthful—
and tender—beef
to your table.*

*This Piedmontese-
Hereford crossbred
calf displays classic
double muscling
because it inherited a
defective myostatin
gene from both of its
parents.*

More than a century ago, European ranchers produced beefy, well-muscled cattle through selective breeding—without understanding how or why their genetic tinkering worked. In the 1990s, several Agricultural Research Service (ARS) scientists, after years of searching for the reason, helped pinpoint a major gene in cattle responsible for boosting muscle size and leanness.

Since then, ARS researchers have added to their understanding of this gene, which codes for the protein myostatin, with the ultimate goal of providing consumers with cuts of beef that are not only lean, but also tender. They work to provide ranchers with information and technology needed to produce such beef profitably and sustainably.

Myostatin limits muscle growth in cattle—and in humans. If the gene responsible for producing myostatin is altered so that it makes an inactive form of the protein, or the gene is intentionally suppressed, the result is more muscle and less fat. ARS researchers are working to find optimal ways to use this gene—alongside others—to make beef more healthful, without sacrificing taste and tenderness.

Love Meat Tender

A benefit of inactivated myostatin—and one likely to be popular with consumers—is beef that's more tender. "Previous researchers tested just the rib eye cut. But we found that with the altered myostatin gene, all cuts of beef have improved tenderness," says Tommy L. Wheeler, a food technologist at ARS's Roman L. Hruska U.S. Meat Animal Research Center (MARC) in Clay Center, Nebraska. Now low-quality cuts of beef, which are usually tough, can be palatable and tender.

And it's not just consumers who benefit. "Even if their cattle have just one copy of the modified gene, ranchers can experience a 7-percent yield increase in salable carcass," says Wheeler.

Production of leaner beef is also more energetically efficient. "But most cattle produced in the United States still contain nearly twice the amount of carcass fat considered optimal," says Michael D. MacNeil, an animal geneticist at ARS's

Fort Keogh Livestock and Range Research Laboratory in Miles City, Montana. This is because the current grading system pays top dollar for beef that contains more marbling—and might be more tender—despite consumer preference for lean beef. Thus, production of lean and tender beef could be a big advantage for ranchers.

Handle With Care

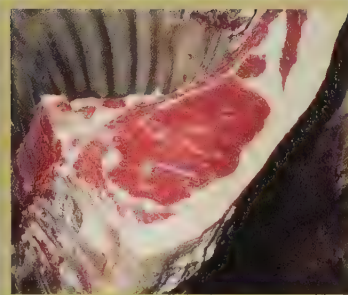
Myostatin manipulation seems like a promising genetic tool, but it requires a level of caution. A condition known as double muscling occurs in animals that inherit a defective myostatin gene from both parents. “Double-muscled calves are extremely muscular at birth, leading to difficulty in exiting the birth canal,” says MARC animal geneticist Timothy P.L. Smith. Even after a successful birth, calves that can’t produce active myostatin are less likely to survive.

Inheriting two copies of the gene producing inactive myostatin can also reduce fertility and decrease the pelvic area of females, which may further contribute to birthing problems. Double-muscled animals can also have a lower tolerance for stress. Because of these problems, some countries now ban use of cattle with double muscling.

ARS research hopes to continue to shed light on the gene, particularly in the context of beef production. “We probably know the major effects of myostatin, but some of its minor ones are still unknown,” says MacNeil. One desirable approach is to cross bulls having genes that make only inactive myostatin with cows having genes that make only the active form.

The gene that codes for the inactive form of myostatin is found more often in breeds like Piedmontese and Belgian Blue. Researchers can cross these lean, well-muscled breeds with ones traditionally used for beef production, such as Angus and Hereford. The resulting animal yields beef cuts lower in saturated fat, satisfying many health-conscious consumers. These crossbred cattle also grow faster than animals that are 100 percent Piedmontese or Belgian Blue, assuring breeders and ranchers maximum returns.

M.A.R.C. (K11279-1)



M.A.R.C. (K11279-3)



M.A.R.C. (K11279-2)



Differences in lean-to-fat ratios are apparent in the marbling within these cuts of meat from cattle having no (top), one (center), or two copies (bottom) of the myostatin gene.

Other Ways To Get Lean

For all the benefits—and problems—associated with the myostatin gene, genetic factors contribute to only about half of what determines tenderness and leanness. Environmental and physical factors, such as feed type, length of time on feed, animal stress, carcass processing technology, and cooking methods, also factor in.

To produce more-healthy beef, researchers and breeders can also look to Limousin and Charolais cattle, which naturally have a strong genetic potential towards lean tissue. It appears that these animals achieve their leanness as a re-

sult of several genes, each exerting a small effect. ARS research is evaluating strategies to use these breeds, as well as those that produce inactive myostatin, to best meet production needs and consumer demands.

To further flesh out understanding of the genes that relate to fat deposition, MacNeil is studying animals not usually found on U.S. ranches—Wagyu cattle. This Japanese breed is associated with the highly marbled luxury known as Kobe beef, which contains up to 45 percent fat. The experimental cattle made their way to Miles City in 1999 after a research farm at Washington State University was closed.

In crossing Wagyu cattle with Limousin cattle, MacNeil, colleague Lee Alexander, and university partners created a genetic resource they can tap for more clues about the genes that play a role in deposition of fat and fatty acid composition.

Wheeler and his MARC colleagues, including Steven Shackelford and Mohammad Koohmaraie, compared Wagyu to other breeds and found that they possess carcass and meat-quality traits very similar to Angus when produced in typical U.S. production systems. Wagyu cattle not destined to become Kobe beef yield leaner carcasses than Angus and other British breeds, but they also grow more slowly and less efficiently than other breeds.—By **David Elstein** and **Erin Peabody**, ARS.

This research is part of Food Animal Production, an ARS National Program (#101) described on the World Wide Web at www.nps.ars.usda.gov.

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Working Towards a Consistently **Tender** Steak

Imagine enjoying a delicious, tender steak at the finest restaurant in the region. Now, imagine eating an equally tender steak at the greasy old diner around the corner. In the future, that may happen thanks to work by Agricultural Research Service (ARS) scientists to make steaks consistently tender.

“Tenderness is the most important trait to consumers,” animal physiologist Mohammad Koohmaraie explains, “and the most variable.”

Koohmaraie leads a group of scientists at the ARS Roman L. Hruska U.S. Meat Animal Research Center (MARC) in researching biochemical mechanisms that make the meat of certain cattle tender and then trying to breed bulls that should sire guaranteed-tender offspring.

The MARC group started making some significant discoveries in the mid 1980s at the Clay Center, Nebraska, laboratory. Koohmaraie and food technologist Tommy L. Wheeler found that the tenderness of meat changes during postmortem aging—first going through a toughening phase before the tenderization phase begins.

Right after slaughter, meat is tender. But for the next 12 hours or so, rigor mortis takes place, stiffening the muscles and making the meat tough. Toward the end of the toughening phase, while the carcass is hanging in a cooler, the tenderization phase begins, which makes most meat—but not all—suitably tender.

The researchers found that tenderization was caused by the enzyme μ -calpain degrading some muscle proteins. They believe industry shouldn't sell meat before it has aged for 14 days, because the postmortem research found that before that time, steaks are more likely to be tough. But those extra days add considerable cost to production because of the requirements for space and controlled temperature.

Koohmaraie explains that not all meat reaches the same level of tenderization. His group wanted to find out why some meats become more tender while others stay too tough. First, through protein chemistry and electron microscopy, they found that μ -calpain breaks down muscle proteins, making meat

tender. Because the calpain enzyme requires calcium for this activity, Koohmaraie and Wheeler developed a way of injecting calcium into meat to help the tenderization process along. This marination technique could be used to produce meat that has both improved tenderness and juiciness.

Doing more research, Koohmaraie and food technologist Steven D. Shackelford found that although μ -calpain causes the protein degradation that improves tenderness, it's actually the activity of a protein called calpastatin that determines how much calpain is active—and thus how tender the steak will be. “The most significant part of this project was learning that it's calpastatin—not calpain—which controls tenderness,” Koohmaraie says.

Since that discovery, other ARS and non-ARS laboratories have confirmed that the calpastatin system indeed greatly influences how tender steaks are. But attempts to develop a tenderness classification system based on calpastatin activity have

STEPHEN AUSMUS (K11703-1)



Food technologists Tommy Wheeler (left) and Stephen Shackelford (middle) prepare muscle for calpain extraction as physiologist Mohammad Koohmaraie separates calpain and calpastatin from a meat extract.

not been successful. This is because calpastatin explains just 45 percent of the variation in tenderness, which is not high enough for accurate classification.

Koohmaraie's collaborators at MARC, chemist Timothy P.L. Smith and geneticist Eduardo Casas, have taken a complementary genetic approach to studying the μ -calpain system. They used a large population of crossbred cattle to identify genes influencing tenderness. They found that variation in the gene that produces μ -calpain appears to affect tenderization.

"We're using genetics to identify DNA markers that can track variation in the calpain gene," Smith says, "and we're looking for DNA tests that can predict the likelihood that a given animal will produce tender meat." This will permit breeding cattle that ranchers will know are more likely to produce consistently tender offspring.

The researchers have made some progress. By sequencing the gene that produces μ -calpain in both tender and tough cattle,

STEPHEN AUSMUS (K11704-1)



Mohammad Koohmaraie loads a muscle extract onto an ion-exchange chromatography column to isolate calpain and calpastatin.



Smith and Casas identified differences that can be used as DNA markers. They have released a DNA test that was effective in identifying tough animals among a large herd of beef cattle representing the most popular beef breeds in the United States. The researchers continue to develop additional markers for use in other breeds.

And since research indicates that there may be many genes other than μ -calpain and calpastatin that influence tenderness—each having a relatively small effect—Smith and Casas warn that more genetic markers will be required to explain enough of the variation to accurately guide breeding choices.

Koohmaraie and Smith stress that tenderness is only about half due to genetics of the animal; the rest is the result of non-genetic, environmental factors such as stress or diet. "There is only so much we can do with genetics," Smith says. The rest is determined by how the animal and the meat are handled throughout the various steps of beef production.

About 10 years ago, Koohmaraie, Shackelford, and Wheeler developed a tenderness classification system that determines the quality from individual animals. It's been used by some beef processors and retailers to market a guaranteed-tender product line. An updated system is expected soon.—By **David Elstein, ARS.**

This research is part of Food Animal Production, an ARS National Program (#101) described on the World Wide Web at www.nps.ars.usda.gov.

Mohammad Koohmaraie, Timothy P.L. Smith, Steven D. Shackelford, Tommy L. Wheeler, and Eduardo Casas are with the USDA-ARS Roman L. Hruska U.S. Meat Animal Research Center, Spur 18D, Clay Center, NE 68933; phone (402) 762-4100, fax (402) 762-4149, e-mail koohmaraie@email.marc.usda.gov, smith@email.marc.usda.gov, shackelford@email.marc.usda.gov, wheeler@email.marc.usda.gov, casas@email.marc.usda.gov. ★

Unraveling the Genome of the Honey Bee, Pig, Cow, and Chicken

An Agency Effort To Sequence Genomes

Though mapping the human genome received a lot of media attention, scientists have been performing the same studies in other animals—with much less fanfare. Researchers from around the world are mapping, or have mapped, the genomes of several farm animals. In addition to helping with the study of agriculture, this work may help further the understanding of human health.

It's not a simple process to map and sequence the genome of an animal. It takes years to do the research. And it takes plenty of money. The National Institutes of Health's (NIH) National Human Genome Research Institute has contributed tens of millions of dollars to various sequencing centers working on other animal genomes. The U.S. Department of Agriculture's Agricultural Research Service (ARS) and Cooperative State Research, Education, and Extension Service have also contributed millions, as have universities and foreign governments.

"In the long run, it makes great business sense for all these organizations to fund genomic research," says Ronnie D. Green,

STEPHEN AUSMUS (D007-1)

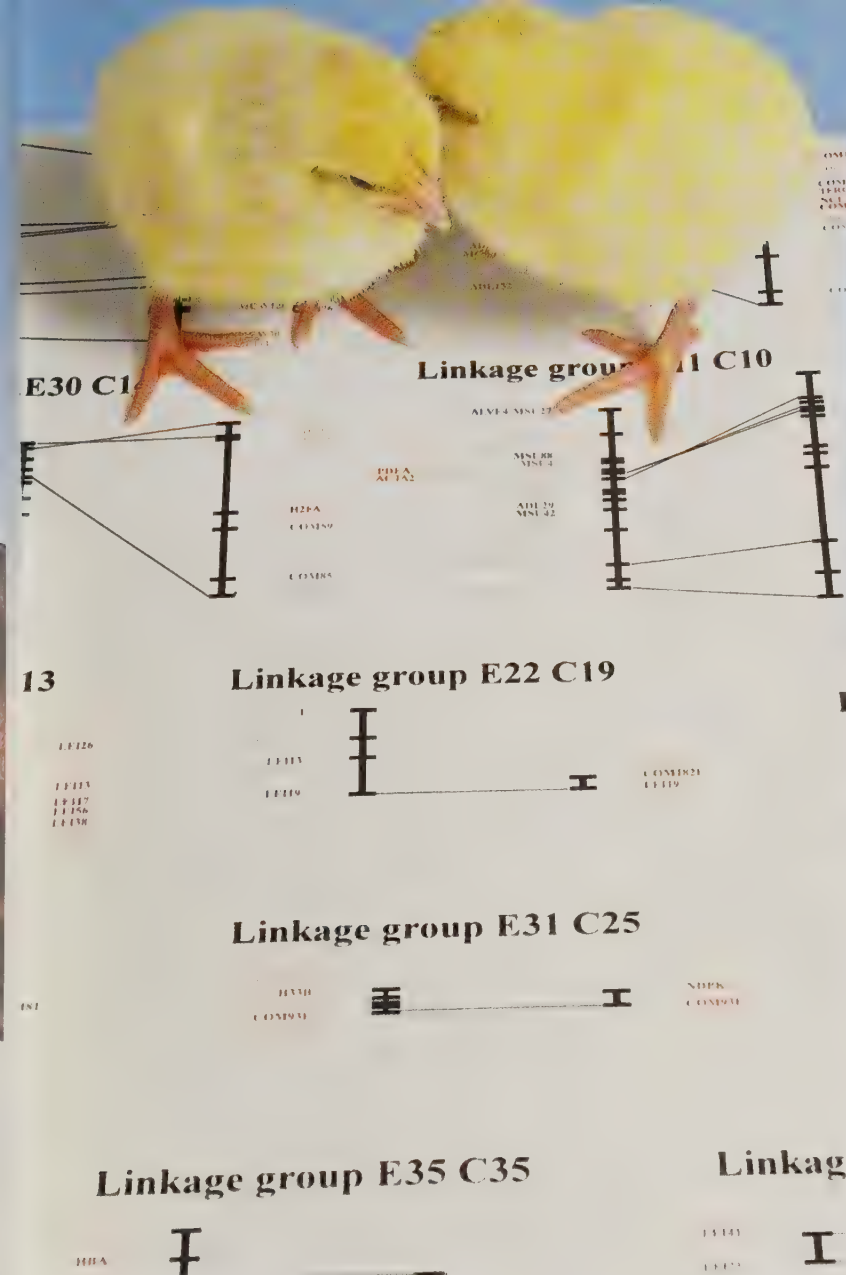


Worker bees remove the mummified remains of larvae infected by the chalkbrood fungus *Ascosphaera apis*. ARS scientists are using the completed bee genome to help understand bee responses to the disease.

STEPHEN AUSMUS (D010-1)



ARS scientists and cooperators throughout the world are in the final stages of completing a bacterial artificial chromosome map of the cow. From this map, the cow genome is already being sequenced. The genome should be useful for selecting cows that resist disease or require less feed.



Chicks atop a picture of a genetic map of a chicken. The new chicken genome will make it much easier to locate genes, especially those for complex traits like disease resistance.

ARS national program leader for Food Animal Production and leader of ARS animal genomic research.

ARS scientists are working with collaborators to map the chicken, honey bee, cow, and pig genomes to learn more about these animals and what information they can provide for the study of humans.

The “Original Chicken” Donates Blueprint to Science

The campus of Michigan State University is home to Female #256, the Red Jungle Fowl (*Gallus gallus*) chicken whose blood samples gave researchers the 1 billion DNA units needed to create the first high-quality draft sequence of the chicken genome. She appears no worse for wear, despite her advanced age of 7 years. Wild Red Jungle Fowl are the ancestors of today’s chickens. The breed has survived at large for about 8,000 years—rare for a wild ancestor of a domesticated animal.

STEPHEN AUSMUS (K11699-1)

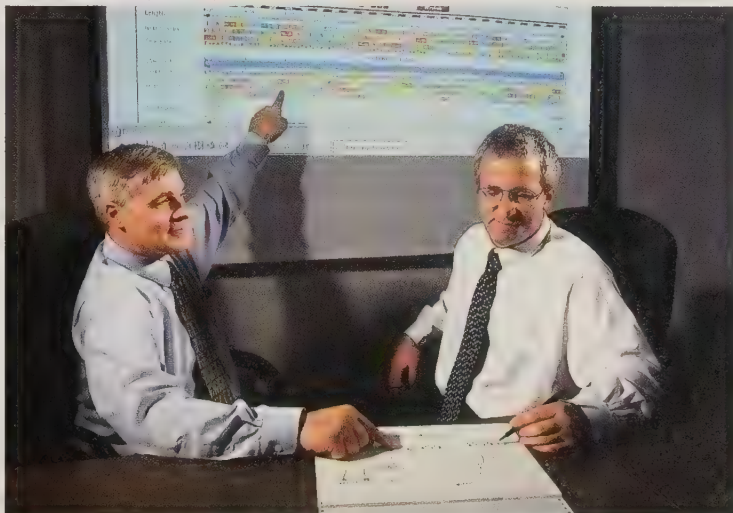


Chemist Tim Smith and cattle wrangler Randy Scott record growth and health data of a heifer to look for correlation of DNA markers and performance at the U.S. Meat Animal Research Center in Clay Center, Nebraska.

Chickens were chosen for mapping because they are the premier nonmammalian vertebrate model organisms. They’re one of the primary models for embryology and development since they grow inside an egg rather than a mother’s uterus, making for easier study. Chickens are also a major model for research on viruses and cancer.

The framework for this genome sequence came from Jerry Dodgson, a molecular biologist at Michigan State University at East Lansing, and ARS geneticist Hans H. Cheng and colleagues at the nearby ARS Avian Disease and Oncology Laboratory.

STEPHEN AUSMUS (K11698-1)



Molecular biologists Steve Kappes (left) and John Keele use gene sequences and genomic sequence to assemble sequences and determine bovine gene structure and regulatory sites.

A genetic map is like an interstate map. A physical map is like a local street map. Use of genetic markers allows comparison of the two.

STEPHEN AUSMUS (D008-1)

Dodgson created a physical map with Female #256's DNA. Cheng created a genetic map using DNA from progeny of Male #10394—a member of the same Red Jungle Fowl line—and a White Leghorn female from an experimental inbred line of chickens. The team used these two maps as the basis for sequencing chicken genes.

NIH funded the project, and the sequence is now online at www.ncbi.nlm.nih.gov/genome/guide/chicken.

A genetic map is a broad overview that shows the order of genes. A physical map shows the actual distance between genes. Using a driving analogy, the genetic map is like an Interstate map, and the physical map is like a local street map. Use of common genetic markers as landmarks allows for integration of the two types of maps. Aligning the genetic map with the genome sequence greatly facilitates scientific efforts to determine the function of each gene and how it influences traits.

At East Lansing, ARS maintains more than 50 inbred lines of chickens ideally suited for genetic studies. The collection—begun in the 1930s—is one of the best in the world.

Over the years, many universities have given up their living collections because maintenance costs were too high. Cheng says, "It's ironic that when the best tool for genetically analyzing these lines arrived, many universities no longer had the chickens around to analyze."

Cheng says that the new genome map to guide the search for genes makes a night-and-day difference. He went almost overnight from having 2,000 genetic markers to having potentially 3 million.

"This map makes it much easier to find genes—especially those for complex traits like disease resistance," he says. "It eliminates a lot of guesswork. It's like suddenly having the complete 'parts list' for a chicken."

Before the map, Cheng had found what he thinks are three genes that confer resistance to Marek's disease, his chief interest. "This genome sequence will be an immense help in finding the rest of the resistance genes," Cheng says. "We found the genes using a unique, integrated functional genomics approach that combines DNA, RNA, and protein methods. The genome sequence will only enhance our power and accuracy."

He expects many other payoffs, including improved vaccines for Marek's and other serious diseases. "We'll also learn how to grow a more nutritious, tastier, and healthier chicken,"



The chip that geneticist Gary Rohrer is holding allows him to evaluate more than 380 pigs for genetic variations at 6 different regions of the genome. This information will help determine which genes affect reproduction in pigs.

Cheng says. "From the ARS viewpoint, mapping and sequencing the chicken genome makes sense because poultry and egg products are a \$25 billion industry and poultry is the number-one meat consumed in the United States."

Sweet Research

ARS scientists have been on the forefront of research both to breed a better honey bee and to manage the welfare and productivity of this important insect.

Humans have a vested interest in *Apis mellifera*; the honey bee's pollination of 90-plus flowering crops results in yield and quality improvements worth more than \$14 billion annually. And don't forget the delectable byproduct of such pollination: honey.

Many dangers, from blood-sucking mites to disease organisms, constantly threaten to undermine the honey bee's efforts, keeping scientists on a fast-track search for new ways to safeguard the insect—and agriculture, no less. Now, a rough draft of *A. mellifera*'s genome is at hand, and bee researchers are gobbling up the wealth of information.

"As an organism whose social order rivals our own in many ways, the honey bee will serve as a natural system for further agricultural studies, including social behavior, cognition, and immune system function," Joseph Jen,

STEPHEN AUSMUS (D005-1)



The bacterium *Paenibacillus larvae* causes American foulbrood disease. Entomologist Jay Evans and technician Tamiaka Armstrong use genomic data to define honey bee genes involved in resistance to the bacterium.

Under Secretary for USDA's Research, Education, and Economics, noted shortly after the genome draft's January 2004 completion.

The honey bee's entire blueprint for life is only about one-tenth the length of the human genome. Still, writing that first draft was no easy task; the feat took a dedicated team of scientists—led by Baylor College of Medicine in Houston—about a year to complete using the latest in genome-sequencing technology and several million dollars in funding.

Kevin Hackett, ARS's national program leader for bees and pollination in Beltsville, Maryland, lists some of the exciting new research avenues that the honey bee genome has opened up: identifying genetic markers to expedite bee-breeding efforts, for example, to improve crop pollination, winter survival, and defensiveness against Africanized bees; host-pathogen modeling studies to better control organisms that cause honey bee diseases; and genome-driven studies to fine-tune honey bee nutrition and pollination.

"If you can locate the 'smelling' genes of bees," says Hackett, "you can use the information to improve their diet through supplementation as well as their ability to forage—with greater pollination resulting."

Jay Evans and Katherine Aronstein, ARS entomologists who participated in the honey bee genome project, are using information from the advance to identify immune system genes that keep bees healthy. Of particular emphasis is characterizing genes involved in potential resistance to the bacterium *Paenibacillus larvae*, which causes foulbrood disease in honey bee larvae. Along with insect pests, parasites, and other pathogens, foulbrood outbreaks in U.S. hives cause \$5 million annually in crop-pollination losses.

At their respective labs in Beltsville and in Weslaco, Texas, Evans and Aronstein are studying a handful of genes and gene products, or proteins, that may stymie honey bee diseases. One tantalizing lead is abaecin, a peptide that honey bees produce to varying degrees when attacked by pathogens.

STEPHEN AUSMUS (D006-1)



**Research
associate
Laura
Decanini and
technician
Andrew
Ulsamer rate
honey bee
colonies for
signs of
disease.**

"We know these bees are responding to foulbrood by producing abaecin," Evans says. "But we're not sure whether a bee that produces more of this peptide is indeed foulbrood resistant."

With the honey bee genome, it's possible to cast a wider net for other such genes and characterize them in hopes of eventually using the information to improve honey bee breeding and management, he adds.

Aronstein has focused her work on a large family of receptors that play roles in the bee's first line of defense against invading microorganisms—what's known as innate, or inborn, immunity.

"The outcome of this genome sequencing research won't give immediate results to the beekeeping industry," says Aronstein. "But it's long-term research with huge potential for a better understanding of bee biology and improvement of management practices."

Studying the Cow Genome

Steven M. Kappes, now ARS Deputy Administrator for Animal Production and Protection, was one of the leaders of ARS's work on the bovine genome at Clay Center, Nebraska. As director of the Roman L. Hruska U.S. Meat Animal Research Center, Kappes worked with a dozen ARS scientists plus many from around the world in developing the physical, bacterial artificial chromosome—BAC—map of the cow.

The scientists first started this project in spring 2000 and are in the final stages of putting the map together.

Though the scientists have not completed the BAC map, researchers are using part of it to sequence the cow genome. "We are already using the BAC map to find DNA markers," Kappes says.

The physical map was developed by researchers in the United States and Australia, Canada, Brazil, France, New Zealand, and the United Kingdom.

Being able to sequence the genome may lead to new knowledge about human health, particularly reproduction traits and immune functions. The knowledge will also obviously help agricultural researchers. Based on evidence from other species, Kappes believes we will be able to find genes that influence feed efficiency in cattle. Cattle producers would use the information to select cows that require less feed. Not only would this reduce the cost of beef production, but it could also mean fewer nutrient and odor problems.

Kappes also notes the possibility of being able to identify cows that are resistant to bovine spongiform encephalopathy—or mad cow disease—by knowing what DNA changes are responsible for the resistance. Then scientists would be able to breed cows naturally immune to the disease.

Many ARS scientists from around the country worked on the cattle genome. Those that had an active role include geneticist Timothy P.L. Smith of the Nebraska lab and Beltsville geneticists Curt Van Tassell and Tad Sonstegard. Van Tassell

found 25 regions in cattle genomes, called quantitative trait loci, that may prove economically important to dairy producers.

Don't Forget the Pigs

Compared to the other animal genomes under study, the pig's has the farthest to go. Animal geneticist Gary A. Rohrer at Clay Center is leading ARS's efforts in sequencing the swine genome. "The sequencing effort is still in its infancy and is evolving as we go," Rohrer explains.

An international consortium has completed the physical map and has started to analyze it. Researchers can view this information at www.sanger.ac.uk/Projects/S_scrofa/. Rohrer believes that it may take 3 to 5 years to complete the actual genome sequencing work.

Rohrer is part of the Swine Genome Sequencing Consortium, which features representatives from governmental agencies and universities from around the world. The group is still develop-

ing strategy on coordinating the eventual sequencing work. They are also working to secure funding for the project.—By **David Elstein, Don Comis, Jan Suszkiw, and Alfredo Flores.**

This research is part of Food Animal Production, an ARS National Program (#101) described on the World Wide Web at www.nps.ars.usda.gov.

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PEGGY GREB (K10974-1)



The high-capacity DNA sequencer being loaded by geneticists Curt Van Tassell (left) and Tad Sonstegard will increase the number of genetic markers available for screening in livestock populations.

Sheep May Happily Graze on Spurge

More than 5 million acres of the western rangeland in America are now overgrown with leafy spurge, greatly reducing the land's plant diversity and productivity. There's something about this noxious weed that makes it repel cattle, horses, and some sheep. But other sheep don't seem to mind its sticky, milky sap and will graze on it with enthusiasm.

Scientists interested in developing an array of nonchemical, spurge-curbng measures are considering using spurge-browsing sheep to help keep the weed in check. They've been closely observing the feeding habits of individual animals to single out those that find it most acceptable. They think there may be a genetic code responsible for chemical sensitivity in sheep and other mammals. By identifying these genes, researchers may be able to build flocks of spurge-loving sheep. *Steven S. Seefeldt and Brent W. Woodward, USDA-ARS U.S. Sheep Experiment Station, Dubois, Idaho; phone (208) 374-5306, e-mail sseefeldt@pw.ars.usda.gov, bwoodward@pw.ars.usda.gov.*

Ghrelin: Key to Chickens' Appetite?

To improve poultry breeding and management practices, scientists are looking for a better understanding and regulation of the genes associated with birds' feed intake and energy balance. They do not yet have a complete understanding of the genetic basis for the regulation of appetite and metabolism in chickens and turkeys. But they moved closer when it was discovered that while the hormone ghrelin boosts appetite in humans, it may have the opposite effect in poultry.

Now scientists have sequenced portions of the gene that produces ghrelin in chickens and turkeys. They are also exploring specific genetic differences between egg-laying and broiler chickens that might account for the significant differences in appetites exhibited by the two types of birds. Selective breeding for lines of chickens and turkeys that grow faster and produce more meat than previous generations has resulted in some unintended changes in feed intake and body composition. Given free access to feed, modern commercial strains of broiler chickens tend to overeat, which can lead to obesity and other health problems. This research may provide insights into controlling or preventing the occurrence of these health concerns. *Mark P. Richards, USDA-ARS Growth Biology Laboratory, Beltsville, Maryland; phone (301) 504-8892, e-mail richards@anri.barc.usda.gov.*

From Sheep Genes to Human Genes

A mutated sheep gene co-discovered with scientists at Duke University may provide clues to the roles of certain genes in human health. Named "*callipyge*," the gene was found in a flock of Oklahoma sheep in the early 1980s. Its expression gave the animals large muscling in their loins and legs. The feature was the result of expression of a normal copy of a specific gene from the mother and a mutated copy of the same gene from the father—an inheritance pattern known as paternal polar overdominance. This was its first known occurrence in a mammalian species.

This research shows the value of obtaining genomic sequences of more agricultural species to align with the human genome in the search for novel genes. Alignment of genomic sequences from several species could help identify important genetic regions not previously recognized in the human genome. This is especially true for regions containing mutations in livestock that have a major impact on the animal, such as the *callipyge* sheep gene. *Bradley A. Freking, USDA-ARS Genetics and Breeding Research Laboratory, Clay Center Nebraska; phone (402) 762-4278, e-mail freking@email.marc.usda.gov.*

The major focus of agriculture is the need to increase food production to meet a growing world population. In the United States, two-thirds of our protein consumption and one-third of our energy requirements are met by foods of animal origin. The world is quickly moving to a global marketplace. Many peoples of the world have profited from free market trade and have become more affluent as a result. These people want greater access to animal products. As a result of increasing demand for access to animal protein and as per-capita income rises in industrialized and developing nations, there is an escalating national and international market for food of animal origin. In some areas of the world, the demand will be difficult to meet because of the lack of well-adapted germplasm and inefficiency of animal production. Advanced molecular tools and a new understanding of animal genomes offer great hope for finding new ways to overcome these problems and more effectively produce nutritious and safe animal products.

The U.S. livestock industry is a multibillion-dollar enterprise with annual farmgate receipts of approximately \$96.8 billion, accounting for over half of all U.S. agricultural receipts. In the past 20 years, the rise in metric tons of food animals produced in the United States has been extraordinary, with the concomitant value of animal production to the United States having equally skyrocketed.

The U.S. Department of Agriculture, Agricultural Research Service's Food Animal Production National Program is charged with conducting cutting-edge research to contribute to increased efficiency and sustainability of production of beef and dairy cattle, poultry, swine, and sheep. Research efforts in the animal sciences over the past century have had dramatic impacts on animal agriculture both in terms of improved biological and economic efficiency of production and in terms of quantity, quality, and safety of animal products. Many major challenges remain, however, requiring the dedicated focus of long-term research teams, particularly in the areas of reproductive longevity and well-being, product quality, reduction of feed and energy inputs, enhancements in nutrient retention, and reduction of negative environmental impacts.

Research is conducted by 91 full-time, permanent scientists at 17 U.S. laboratories. The annual budget of the program is approximately \$40 million. These efforts are highly leveraged by cooperative research between USDA-ARS scientists and a number of university, industry, and other Federal agency partners.

ARS food animal production research supports Strategic Goal 1—Enhance Economic Opportunities for Agricultural Producers—of the USDA Research, Education, and Economics (REE) Strategic Plan 2003-2008 and contributes to the following performance measures:

- 1.2.1. Provide producers with scientific information and technologies that increase production efficiency, develop improved germplasm, safeguard the environment, improve animal welfare, and reduce production risks and losses
- 1.2.2. Develop needed information on the relationships between nutrients, reproduction, growth, and conversion to and marketability of animal products
- 1.2.3. Identify genes responsible for economically important traits, including animal product quality, efficiency of nutrient utilization, and environmental adaptability
- 1.2.4. Maintain, characterize, and use genetic resources to optimize and safeguard genetic diversity and promote viable, vigorous animal production systems

Activities of this national program are carefully coordinated with activities in a number of other ARS national programs—including animal health, animal well-being and stress control systems, rangelands, pastures and forages, waste management and byproduct utilization, food safety, human nutrition, air quality, and quality and utilization of agricultural products—and with the corresponding research programs of USDA's Cooperative State Research, Education, and Extension Service (CSREES).

Research activities in the program operate on a 5-year cycle, with the current projects authorized from 2002 to 2007. These projects contribute to a defined national program action plan that was developed in 2001 based on extensive input and priority setting with a wide range of customers and stakeholders of the agency, including industry, nongovernmental organizations, academia, regulatory agencies, and other Federal research organizations. An outline summary of this action plan is presented below.

Vision Statement

Sustain food animal productivity and profitability through application of technology and management to improve genetic and reproductive performance.

Mission Statement

The mission of the Food Animal Production Program is to protect, evaluate, identify, and develop biotechnological methods to use animal germplasm and associated genetic and genomic repositories and databases to ensure an abundant and safe supply of animal products at a price that is competitive in the United States and foreign markets.

Research Components

Reproductive Efficiency

- Environmental effects
- Fertile gamete production
- Gamete and embryo storage, sexing, cryopreservation, and use
- Embryo, fetal, and neonatal development and survival
- Interactions of endocrine and immune systems

Conservation, Characterization, and Use of Genetic Resources

- Characterizing genetic resources
- Preserving genetic resources
- Information systems

Genetic Improvement

- Developing breeding objectives
- Accelerating selection response
- Improving health and well-being
- Transgenic livestock and poultry

Genomic Tools

- Comprehensive maps
- Genotyping systems
- Tools and reagents
- Genomic enhancement systems
- Bioinformatics and statistical analysis tools

Nutrient Intake and Use

- Regulating gene function
- Interactions affecting reproduction
- Microbial effects
- Minimizing production losses
- Nutrient use and feed evaluation

Growth and Development

- Regulating feed intake
- Tissue growth and development

Product Quality

- Interactions of genetics and nutrition
- Biological mechanisms controlling variation
- Predicting product quality or defects

Integrated Systems

- User information packages

Promising Future

This is a particularly exciting time for the food animal production program area. In 2004, draft DNA genome sequences were released into the public domain for the chicken and the cow. Success in obtaining the needed funding for sequencing of the swine genome was announced in January 2005, with the launch of the project expected to occur by year's end. In all three of these genome projects, a significant portion of the deliverables have been additional tools and reagents that will allow research to move into areas previously not possible, which include efficiency of feed utilization, genetic adaptation to environmental stressors, and reproductive efficiency. Major long-term efforts are now yielding results in building infrastructure in the agency for bioinformatics, functional genomics, proteomics, metabolomics, and meta-genomics. These efforts have required creative approaches to funding and leveraging of resources across Federal agencies, international governments, and private industry. These developments have opened a new frontier for research in food animal production and coincidentally have elevated the expectations of the future impact of this program.

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ARS FOOD ANIMAL PRODUCTION RESEARCH

